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Gencore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 16:50:38 : Search time 22 seconds
(without alignments)
2801.007 Million cell updates/sec

Title: US-09-646-835-1

Sequence: 1 MAAKMAIGIDIGTTYSYGV.....FGAGKSGSGSCRTIEVD 641

Scoring table:

gapop 60.0 , dapept 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :
1: PIR:73:*
2: PIR:*
3: PIR:*
4: PIR:*

Prod. No. is the number of results predicted by chance to have a score greater than the observed score, being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	641	100	641	A45871	dnak-type molecule
2	641	64.3	640	A29160	dnak-type molecule
3	370	57.7	641	S53157	dnak-type molecule
4	209	32.6	641	S35158	dnak-type molecule
5	175	27.3	638	S31766	dnak-type molecule
6	114	17.8	641	S54942	dnak-type molecule
7	101	15.8	642	JH0095	dnak-type molecule
8	95	14.5	420	A26883	dnak-type molecule
9	65	12.5	633	S10859	dnak-type molecule
10	55	8.6	633	S10859	dnak-type molecule
11	55	8.6	633	S10859	dnak-type molecule
12	55	8.6	634	A25646	dnak-type molecule
13	55	8.6	639	A55719	dnak-type molecule
14	55	8.6	641	149761	dnak-type molecule
15	55	8.6	641	S41115	dnak-type molecule
16	54	8.4	640	T43724	dnak-type molecule
17	54	8.4	646	S07197	dnak-type molecule
18	53	8.3	646	A35922	dnak-type molecule
19	53	8.3	646	JC4853	dnak-type molecule
20	53	8.3	646	A27077	dnak-type molecule
21	53	8.3	646	A31716	dnak-type molecule
22	53	8.3	647	A45972	dnak-type molecule
23	53	8.3	647	A45972	dnak-type molecule
24	53	8.3	650	S11456	dnak-type molecule
25	53	8.3	651	A36333	dnak-type molecule
26	50	7.8	372	PO0138	hypothetical prote
27	48	7.5	646	B86295	dnak-type molecule
28	48	7.5	125	137564	dnak-type molecule
29					

ALIGNMENTS

Query Match	Similarity	100.0%	Score	641:	DB 2:	Length	641:
Best Local	Similarity	100.0%	Prod. No. 0:				
Matches	641:	Conservative	0:	Mismatches	0:	Indels	0:
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DB	1	MAAKMAIGIDIGTTYSYGV.....FGAGKSGSGSCRTIEVD	641	MAAKMAIGIDIGTTYSYGV.....FGAGKSGSGSCRTIEVD	641	MAAKMAIGIDIGTTYSYGV.....FGAGKSGSGSCRTIEVD	641
QY	61	LNPOVTFENKRLIGKRGKQPVYOSDMKMFVYINGDKRKVOVSYKGTAAAYEETS	120	LNPOVTFENKRLIGKRGKQPVYOSDMKMFVYINGDKRKVOVSYKGTAAAYEETS	120	LNPOVTFENKRLIGKRGKQPVYOSDMKMFVYINGDKRKVOVSYKGTAAAYEETS	120
DB	61	LNPOVTFENKRLIGKRGKQPVYOSDMKMFVYINGDKRKVOVSYKGTAAAYEETS	120	LNPOVTFENKRLIGKRGKQPVYOSDMKMFVYINGDKRKVOVSYKGTAAAYEETS	120	LNPOVTFENKRLIGKRGKQPVYOSDMKMFVYINGDKRKVOVSYKGTAAAYEETS	120
QY	121	SNVTFKKKEIAEAVLGYPVNAVITYPAVFDMSOQAFADGAVIAGLVLRINEPTAA	180	SNVTFKKKEIAEAVLGYPVNAVITYPAVFDMSOQAFADGAVIAGLVLRINEPTAA	180	SNVTFKKKEIAEAVLGYPVNAVITYPAVFDMSOQAFADGAVIAGLVLRINEPTAA	180
DB	121	SNVTFKKKEIAEAVLGYPVNAVITYPAVFDMSOQAFADGAVIAGLVLRINEPTAA	180	SNVTFKKKEIAEAVLGYPVNAVITYPAVFDMSOQAFADGAVIAGLVLRINEPTAA	180	SNVTFKKKEIAEAVLGYPVNAVITYPAVFDMSOQAFADGAVIAGLVLRINEPTAA	180
QY	181	IANGDRTKGRBNVLPDLAGGTFDVSITLIDDIIEVKAAGDTHLGGEDPBNLVNH	240	IANGDRTKGRBNVLPDLAGGTFDVSITLIDDIIEVKAAGDTHLGGEDPBNLVNH	240	IANGDRTKGRBNVLPDLAGGTFDVSITLIDDIIEVKAAGDTHLGGEDPBNLVNH	240
DB	181	IANGDRTKGRBNVLPDLAGGTFDVSITLIDDIIEVKAAGDTHLGGEDPBNLVNH	240	IANGDRTKGRBNVLPDLAGGTFDVSITLIDDIIEVKAAGDTHLGGEDPBNLVNH	240	IANGDRTKGRBNVLPDLAGGTFDVSITLIDDIIEVKAAGDTHLGGEDPBNLVNH	240
QY	241	FVEEFKRRKHKIDQNKRAVRLRTCEAPRTSSSTOASLEIDSLPEIDPTSTIRA	300	FVEEFKRRKHKIDQNKRAVRLRTCEAPRTSSSTOASLEIDSLPEIDPTSTIRA	300	FVEEFKRRKHKIDQNKRAVRLRTCEAPRTSSSTOASLEIDSLPEIDPTSTIRA	300
DB	241	FVEEFKRRKHKIDQNKRAVRLRTCEAPRTSSSTOASLEIDSLPEIDPTSTIRA	300	FVEEFKRRKHKIDQNKRAVRLRTCEAPRTSSSTOASLEIDSLPEIDPTSTIRA	300	FVEEFKRRKHKIDQNKRAVRLRTCEAPRTSSSTOASLEIDSLPEIDPTSTIRA	300
QY	301	RFEELCSDFRSTLEVERKALDQAKLDNAQIHDLVLVGSSTIRIPKXKLLADPTNGRD	360	RFEELCSDFRSTLEVERKALDQAKLDNAQIHDLVLVGSSTIRIPKXKLLADPTNGRD	360	RFEELCSDFRSTLEVERKALDQAKLDNAQIHDLVLVGSSTIRIPKXKLLADPTNGRD	360
DB	301	RFEELCSDFRSTLEVERKALDQAKLDNAQIHDLVLVGSSTIRIPKXKLLADPTNGRD	360	RFEELCSDFRSTLEVERKALDQAKLDNAQIHDLVLVGSSTIRIPKXKLLADPTNGRD	360	RFEELCSDFRSTLEVERKALDQAKLDNAQIHDLVLVGSSTIRIPKXKLLADPTNGRD	360
QY	361	KSINDEAVAGAAVOAALIMGDKSENWODLLDLVAPSLGLETFAGVWFLTKENST	420	KSINDEAVAGAAVOAALIMGDKSENWODLLDLVAPSLGLETFAGVWFLTKENST	420	KSINDEAVAGAAVOAALIMGDKSENWODLLDLVAPSLGLETFAGVWFLTKENST	420
DB	361	KSINDEAVAGAAVOAALIMGDKSENWODLLDLVAPSLGLETFAGVWFLTKENST	420	KSINDEAVAGAAVOAALIMGDKSENWODLLDLVAPSLGLETFAGVWFLTKENST	420	KSINDEAVAGAAVOAALIMGDKSENWODLLDLVAPSLGLETFAGVWFLTKENST	420

R:Mestrlil, R.; Chi, S.H.; Sayen, M.R.; Dillmann, W.H.
 Biochem. J. 298, 561-569, 1994
 A:Title: Isolation of a novel inducible rat heat-shock protein (HSP70) gene and its expression
 A:Reference numbers: S43388; MUID:94190287; PMID:8441767
 A:Molecule type: DNA
 A:Residues: 1-70; <NG> 73-109; <R> 111-203; <P> 205-261; <P> 263; <ADGV> 268-641 <MES>
 A:Cross-references: EMBL:X15357; NID:9407163; PDB:1CA53140.1; PID:9407164
 A:Experimental source: Isochaemic rat heart
 R:Ilsovska, K.; Midlak, M.; Kravetz, Z.; Molnyczek, P.; Wisniewski, J.
 Biochim. Biophys. Acta 1219, 64-72, 1994
 A:Reference numbers: S47522; MUID:94368874; PMID:8086479
 A:Accession: S47522
 A:Molecule type: DNA
 A:Residues: 1-70; <NG> 73-407; <R> 409-641 <LIS>
 A:Cross-references: EMBL:X14271; NID:93413498; PDB:1CA52328.1; PID:9396270
 A:Note: the authors translated the codon CCG for residue 365 as ASP
 R:Longo, F.R.; Wang, S.; Nageswami, P.; Zhang, J.S.; Chen, J.; Massa, S.M.; Sharp, F.R.
 A:Title: cDNA cloning and expression of stress-inducible rat hsp70 in normal and injured
 A:Reference numbers: I56574; MUID:94096443; PMID:8271311
 A:Accession: I56574
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-226; <D> 228-641 <QON>
 A:Cross-references: GB:116764; NID:9294567; PDB:1AA17441.1; PID:9294568
 A:Gene: hsp70.1
 A:Genetics: <RSP2>
 A:Gene: hsp70.2
 A:Function:
 A:Description: Involved in protein folding and assembling/dissassembling of protein comp
 C:Keywords: ATP; heat shock; molecular chaperone; stress-induced protein
 C:Superfamily: heat shock protein 70
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 Best Local Similarity 100.0%; Pred. No. 4.e-108;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 313 TLEPERALDKADLNKHIDVYVGSSTRIPKVKYLLDFFNGKDLNSINDEAVANG 372
 Db 313 TLEPERALDKADLNKHIDVYVGSSTRIPKVKYLLDFFNGKDLNSINDEAVANG 372
 Oy 373 AAYOAAIMLMDKSENVODLLIDVAPISLGLFTAGCVMTALIKRSTPTPKOTQ 426
 Db 373 AAYOAAIMLMDKSENVODLLIDVAPISLGLFTAGCVMTALIKRSTPTPKOTQ 426
 RESULT 7
 JH0095
 dnk-type molecular chaperone hsp70 - mouse
 A:Alternate names: heat shock protein 70
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1990 #sequence-revision 31-Dec-1990 #text-change 20-Aug-1999
 C:Accession: JH0095
 R:Hunt, C.; Calderwood, S.
 Gene 87, 339-344, 1990
 A:Reference numbers: MUID:90236310; PMID:2332169
 A:Accession: JH0095
 A:Molecule type: DNA
 A:Residues: 1-642 <HUN>
 A:Cross-references: GB:M35021; NID:9194022; PDB:1AA37864.1; PID:9387211
 A:Experimental source: strain M3
 A:Function: Involved in protein folding and assembling/dissassembling of protein comp
 C:Superfamily: heat shock protein 70
 C:Keywords: ATP; molecular chaperone
 Query Match 15.8%; Score 101; DB 2; Length 642;
 Best Local Similarity 100.0%; Pred. No. 9.9e-95;
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 138 PUTNAVITVAVENSDQROATKACVTAELNATLLEPPTAAATANGDTRGKGRVLL 197
 Db 138 PUTNAVITVAVENSDQROATKACVTAELNATLLEPPTAAATANGDTRGKGRVLL 197
 Oy 198 PDLGGGTDFVSLITIDGCIFFPKATPADPHLGGEDPDRLL 238
 Db 198 PDLGGGTDFVSLITIDGCIFFPKATPADPHLGGEDPDRLL 238
 RESULT 8
 J26283
 dnk-type molecular chaperone - mouse (fragment)
 A:Alternate names: heat shock protein 66
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Nov-1988 #sequence-revision 19-Nov-1988 #text-change 20-Aug-1999
 C:Accession: J26283
 R:Long, D.G.; Moran, L.A.
 Gene 229, 219-222, 1986
 A:Reference numbers: MUID:86111900; PMID:2866009
 A:Accession: J26283
 A:Molecule type: mRNA
 A:Residues: 1-420 <LOW>
 A:Cross-references: GB:M12571; NID:9194014; PDB:1AA57234.1; PID:9387208
 A:Note: the authors translated the codon CCG for residue 173 as VAL and CGC for resid
 A:Description: Involved in protein folding and assembling/dissassembling of protein co
 C:Superfamily: heat shock protein 70
 C:Keywords: ATP; molecular chaperone
 Query Match 12.5%; Score 80; DB 2; Length 420;
 Best Local Similarity 100.0%; Pred. No. 2.4e-73;
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 333 DLIVYGGSTRIPYOKLLDFFNGKDLNSINPEVAVYGAAYOAAIMLMDKSENVODLL 392
 Db 112 DLIVYGGSTRIPYOKLLDFFNGKDLNSINPEVAVYGAAYOAAIMLMDKSENVODLL 171
 Oy 393 LIDVAPISLGLFTAGCVMTA 412
 Db 172 LIDVAPISLGLFTAGCVMTA 191
 RESULT 9
 I79340
 dnk-type molecular chaperone HSP70-2 - human (fragment)
 A:Alternate names: chaperonin HSP70-2; HSC heat shock protein HSP70-2
 C:Species: Homo sapiens (man)
 C:Date: 31-May-1996 #sequence-revision 31-May-1996 #text-change 20-Aug-1999
 C:Accession: I79340
 R:Sargent, C.A.; Dunham, I.; Townsend, J.; Campbell, R.D.
 Proc. Natl. Acad. Sci. U.S.A. 86, 1968-1972, 1989
 A:Reference numbers: I59139; MUID:89184548; PMID:2338825
 A:Accession: I79340
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Residues: 1-65 <RHS>
 A:Cross-references: GB:M4744; NID:9189529; PDB:1AA59845.1; PID:9188530
 A:Genetics: <LIS>
 A:Gene: HSP70-2
 A:Function:
 A:Description: Involved in protein folding and assembling/dissassembling of protein co
 C:Superfamily: heat shock protein 70
 C:Keywords: ATP; molecular chaperone
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 Best Local Similarity 100.0%; Pred. No. 1.1e-58;
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 360 NKSINDEAVANGAAYOAAIMLMDKSENVODLLIDVAPISLGLFTAGCVMTALIKRST 419
 Db 360 NKSINDEAVANGAAYOAAIMLMDKSENVODLLIDVAPISLGLFTAGCVMTALIKRST 419

Db 1 NKSINPEAVATGAAVCAATIMKSEKSENVDDLLLDVAFSLGLETAGVMTALIKRST 60
 420 IPRKG 424
 61 IPRKG 65

RESULT 10

S08211
 dnak-type molecular chaperone hsp70.2 - rat
 N:Alternate names: heat shock protein 70.2; heat shock protein, testis-specific
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 19-Nov-1998 #sequence_revision 07-Sep-1990 #text_change 30-Jan-1998
 C:Accession: S08211
 R:Morimoto, R.I.; Hunt, C.; Huang, S.Y.; Berg, K.L.; Banerji, S.S.
 J. Biol. Chem. 261, 12692-12699, 1986
 A:Title: Organization, nucleotide sequence, and transcription of the chicken HSP70 gene
 A:Reference number: S08211; PMID:90123930; PMID:1688714
 A:Accession: S08211

A:Molecule type: DNA
 A:Residues: 633
 A:Note: The authors translated the codon GAG for residue 217 as Asp

A:Gene: hsp70
 C:Function:
 A:Description: Involved in protein folding and assembling/disassembling of protein comp

A:Superfamily: heat shock protein 70
 C:Keywords: ATP; molecular chaperone

Query Match
 Best Local Similarity 100.0%; Pred. No. 1.5e-47;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

6 AITDILGTTTSCVGVFGKRGVEITANDGKNTTPSYAFTDRLIGDAKKNYA 60
 7 AITDILGTTTSCVGVFGKRGVEITANDGKNTTPSYAFTDRLIGDAKKNYA 61

RESULT 11

S10859
 dnak-type molecular chaperone HSP70.2 - mouse
 N:Alternate names: heat shock protein 70.2
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 30-Jan-1998
 C:Accession: S10859
 R:Zakeri, Z.F.; Wolgemuth, D.J.; Hunt, C.R.
 Mol. Cell. Biol. 8, 2925-2932, 1988
 A:Title: Identification and sequence analysis of a new member of the mouse HSP70 gene fa

A:Reference number: S10859; PMID:88302212; PMID:3405224
 A:Accession: S10859
 A:Molecule type: DNA
 A:Residues: 1-633 <ZAK>
 A:Status: preliminary
 A:Cross-references: EMBL:M20567
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 A:Gene: HSP70.2

A:Description: Involved in protein folding and assembling/disassembling of protein comp

A:Superfamily: heat shock protein 70
 C:Keywords: ATP; molecular chaperone

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 7 AITDILGTTTSCVGVFGKRGVEITANDGKNTTPSYAFTDRLIGDAKKNYA 61

RESULT 12

A25646
 dnak-type molecular chaperone - chicken
 N:Alternate names: heat shock protein 70
 C:Species: Gallus gallus (chicken)
 C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
 R:Morimoto, R.I.; Hunt, C.; Huang, S.Y.; Berg, K.L.; Banerji, S.S.
 J. Biol. Chem. 261, 12692-12699, 1986
 A:Title: Organization, nucleotide sequence, and transcription of the chicken HSP70 ge
 A:Reference number: A25646; PMID:86304452; PMID:3017985
 A:Accession: A25646

A:Molecule type: DNA
 A:Residues: 634 <ZAK>
 A:Note: The authors translated the codon TCG for residue 583 as Trp

A:Gene: hsp70
 C:Function:
 A:Description: Involved in protein folding and assembling/disassembling of protein co

A:Superfamily: heat shock protein 70
 C:Keywords: ATP; molecular chaperone

Query Match
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RESULT 13

A55719
 dnak-type molecular chaperone HSPA2 - human
 N:Alternate names: heat shock protein A2
 C:Species: Homo sapiens (man)
 C:Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 20-Aug-1999
 C:Accession: A55719
 R:Yan, C.E.; Hunt, C.R.; Trask, B.J.; Clancy, K.P.; Weber, J.L.;
 Genomics 2, 85-93, 1994
 A:Title: Cloning, sequencing, and mapping of the human chromosome 14 heat shock prote
 A:Reference number: A55719; PMID:95130116; PMID:7829106
 A:Accession: A55719

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-633 <ZAK>
 A:Cross-references: GDB:126336; MID:q476704; PDB:AAA32698.1; PDB:q476705
 C:Genetics:
 A:Gene: HSPA2

A:Cross-references: GDB:126059; OMIM:140560
 A:Map position: 14q22-14q22
 A:Introns: #status absent

C:Function:
 A:Description: Involved in protein folding and assembling/disassembling of protein co

A:Superfamily: heat shock protein 70
 C:Keywords: ATP; molecular chaperone

Query Match
 Best Local Similarity 100.0%; Pred. No. 1.5e-47;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 7 AITDILGTTTSCVGVFGKRGVEITANDGKNTTPSYAFTDRLIGDAKKNYA 61

RESULT 14

149761
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 N:Alternate names: heat shock protein 70
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
 C:Accession: 149761
 R:Shoek, M.; Olavsen, M.G.; Van Vugt, H.; Milner, C.M.; Teuscher, C.; Campbell, R.D.
 Immunogenetics 40, 159-162, 1994

A:Title: Coding sequences and levels of expression of Hsc70t are identical in mice with
A:Reference number: I49761; MUID:94299288; PMID:8026864
A:Accession: I49761
A:Species: Rattus norvegicus (Rat) (rat)
A:Strain: Frelang
A:Molecule type: translated from GB/EMBL/DBS
A:Residues: 1-641 <RES>
A:Cross-references: GB:I27086; NID:9457299; PIDN:AAA59362.1; PID:9457300
C:Genetics:
A:Gene: Hsc70t
C:Function:
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C:Keywords: ATP; molecular chaperone

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Db

RESULT 15
.S41415
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A:Reference number: S41415
A:Accession: S41415
A:Species: Rattus norvegicus (Rat) (rat)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000
C:Accession: S41415; 168987
R:Putz, W.
submitted to the EMBL Data Library, January 1994
A:Reference number: S41413
A:Accession: S41413
A:Species: Rattus norvegicus (Rat) (rat)
A:Molecule type: DNA
A:Residues: 1-641 <LUT>
A:Cross-references: EMBL:X77209; NID:91814002; PIDN:CAA54424.1; PID:9450934
R:Malter, L.; Raub, F.; Gunther, E.
Immunogenetics 40, 325-330, 1994
A:Title: Comparative analysis of the three major histocompatibility complex-linked heat
A:Reference number: I54542; MUID:95012453; PMID:7927536
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Best Local Similarity 100.0%; Pred.No.1.5e-47;
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Db

Search completed: December 4, 2002, 16:53:11
Job time : 23 secs


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DB 481 DANGLIMVATDKSGKANKTTITNDKGRLSKEEIERMVOAEARKKAEDEVOREEVSANK 540
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DB 541 ALESTAFNRKSAVEDBGLKGISBAUKRYLQKCEVYSIMDLANTLAERDEFEHRKELE 600
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DB 601 QVCNPIISGLYOGAGPGPGFAGPGAGPGSGSGPTIEVD 641

RESUME 2
US-09-761-534A-10
: Sequence 10: Application us/09761534A
: Patent No. US2002014626A1
: GENERAL INFORMATION:
: APPLICANT: Huang, Qian
: APPLICANT: Richmond, Joan F.L.
: APPLICANT: Cho, Bryan K.
: APPLICANT: Smith, Deborah
: APPLICANT: Chen, Jianzhn
: APPLICANT: Elsen, Herman N.
: APPLICANT: Young, Richard A.
: TITLE OF INVENTION: In Vivo CTL Elicitation By Heat Shock
: TITLE OF INVENTION: Protein Fusion Proteins Maps To A Discrete Domain and is
: FILE REFERENCE: CD4-T Cell-Independent
: CURRENT FILING DATE: 2000-01-15
: PRIOR FILING DATE: 2000-12-01
: PRIOR APPLICATION NUMBER: PCT/US00/32831
: PRIOR FILING DATE: 2000-01-14
: NUMBER OF SEQ ID NOS: 25
: SOFTWARE: PatscSD for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 642
: TYPE: PRT
: ORGANISM: Unknown
: FEATURE:
: OTHER INFORMATION: Murine hap70
US-09-761-534A-10

Query Match 95.8%; Score 3125.5; DB 10; Length 642;
Best Local Similarity 95.2%; Pred. No. 1,9e-214;
Matches 611; Conservative 20; Mismatches 10; Indels 1; Gaps 1;

```

```

OY 181 IAVGLDRTGKGERNNVLPFDLGGCTPDVSIJLTIDGIFEVKATAGDTHLGGEDFDNRVLNH 240
DB 181 IAVGLDRTGKGERNNVLPFDLGGCTPDVSIJLTIDGIFEVKATAGDTHLGGEDFDNRVLNH 240
OY 241 FEEERKKRKKDDSONRFAVRRLPTCRRAKRTLSSTQASLTDSIFGCIIDYISITRA 300
DB 241 FEEERKKRKKDDSONRFAVRRLPTCRRAKRTLSSTQASLTDSIFGCIIDYISITRA 300
OY 301 REBELCSDFPSTLPEVERALRDAKIDRAQIHDLVWGSTRIPVOKLLDDEFGNRDLM 360
DB 301 REBELCSDFPSTLPEVERALRDAKIDRAQIHDLVWGSTRIPVOKLLDDEFGNRDLM 360
OY 361 KSIINDEVAAGAAVOAAILMGKSENVOULLLDVAAPLSIGLEFAGGYMALIKRNSSTI 420
DB 361 KSIINDEVAAGAAVOAAILMGKSENVOULLLDVAAPLSIGLEFAGGYMALIKRNSSTI 420
OY 421 PRKQOIFPTTSDNPGVYLIOVEGERAMTKNNLLAREBELSGIPEAPGVPQILETFDI 480
DB 421 PRKQOIFPTTSDNPGVYLIOVEGERAMTKNNLLAREBELSGIPEAPGVPQILETFDI 480
OY 481 DANGLIMVATDKSGKANKTTITNDKGRLSKEEIERMVOAEARKKAEDEVOREEVSANK 540
DB 481 DANGLIMVATDKSGKANKTTITNDKGRLSKEEIERMVOAEARKKAEDEVOREEVSANK 540
OY 541 ALESTAFNRKSAVEDBGLKGISBAUKRYLQKCEVYSIMDLANTLAERDEFEHRKELE 600
DB 541 ALESTAFNRKSAVEDBGLKGISBAUKRYLQKCEVYSIMDLANTLAERDEFEHRKELE 600
OY 601 QVCNPIISGLYOGAGPGPGFAGPGAGPGSGSGPTIEVD 641
DB 601 QVCNPIISGLYOGAGPGPGFAGPGAGPGSGSGPTIEVD 641

RESUME 3
US-09-870-759-43
: Sequence 43: Application us/09870759
: Patent No. US20020177551A1
: GENERAL INFORMATION:
: APPLICANT: TERMAN, David S
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
: FILE REFERENCE: 87/0759 NUMBER: US-09/870,759
: CURRENT FILING DATE: 2002-01-14
: PRIOR FILING DATE: 2000-05-30
: PRIOR APPLICATION NUMBER: US 60/208,128
: NUMBER OF SEQ ID NOS: 166
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 43
: LENGTH: 646
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-870-759-43

Query Match 87.6%; Score 2859.5; DB 9; Length 646;
Best Local Similarity 85.6%; Pred. No. 1.5e-195;
Matches 553; Conservative 48; Mismatches 40; Indels 5; Gaps 3;

```



```

Db 302 QREHSLSLERTKQPCQALNDKSLKSLSDIDYVLGSGKHPANVAVKELF--GKEEN 360
Oy 361 KSLINDEAVAGAAVOALILMGDSKNNOYDILLDVAPLSLGLTACGATMLIKRNSIT 420
Db 361 KQVNDDEVAVGAIAOGVYLSGE---VKVYLLLDVYPLSLGIELTGVMFLVLEHRTI 416
Oy 421 PKRQOIFETYSNDQPGVLTQVYEGEERANTKNNLLGRFELSGTPAPRGVYQVLEVPDI 476
Db 417 PPKQKQYPSYMANQNPATITVYVQSGKPMKNSKELNDITDTPAPMGHQPDLVETFDI 480
Oy 481 DANGILNVTATDQSGKANKTITINDKRSKEELTEMVQAKKKEDEVOERENAKN 540
Db 477 DANGILNVTASAKDASREKRIEIASSS--LKEDIDQMIKIDAELEKKEDEKOEKESDVKN 535
Oy 541 ALESTAFNMKSAYDEGLAKRISDAKKV---LDKQDQYISMLDANTLAK--DEFE- 593
Db 536 EADQKIFRAEKAVYD--YIDRIAPRELYVELEHLEKYNQALK--EDKSTALIKASDELST 592
Oy 594 HRRKELE---QVCNPRIISGLYGGAGGSG-----PGSGAQSGKQSGSG--PTIEPND 641
Db 593 HMOKIGEAQVQASAAASSAANAQGHINSEDLKKHSFSTRPAGSASSTDNIEDAD 652

* RESULT 10
US-09-815-242-12058
; Sequence 12058, Application US/09815242
; Patent No. US20020061559A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Yuskind, Judith W.
; APPLICANT: Winkler, John D.
; APPLICANT: Trawick, John D.
; APPLICANT: Grant, J.
; APPLICANT: Yamamoto, Robert T.
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA, OITA US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-26/2042,578
; PRIOR FILING DATE: 2000-05-26/242,578
; PRIOR FILING DATE: 2000-10-21
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ IDS: 11
; SOFTWARE: PalsBSEQ for Windows Version 4.0
; SEQ ID NO 12058
; LENGTH: 637
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-12058
Query Match 43.88: Score 1430.5; DB 10; Length 637;
Best Local Similarity 49.58; Pred No. 4, 5e-94
Matches 310: Conservative 106; Mismatches 179; Indels 31; Gaps 14;
Oy 7 IDIDLITVYSCGVQFQHGVEIIANDQGNRTTSPSYAFT--DREHLIGDAANQVALLNPN 65
Db 5 IDIDLITVNSCVALLENGWVAVIEABACATTPSIIATYINDGEBTLVQGPABQAVATNPN 64
Oy 66 TVFAKRLIGKRGDPVQSGMKHMPQVYINQDQKRYQSYKGTATYFEELISSWLT 125

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Db 65 TLFAVKRLIGKREENVQKDIQWVYSYK--AKNDMAENYKQKKA--PQISAEVLA 121
Oy 126 KKKELIENYLGPPYNNVITVPAPFNSQKQATDQAGYAGLAVYRIITEPTAAALAYGL 185
Db 122 KKKKTAEDYLGEPVYEAIVTPAVFNSQKQATDQAGYAGLADVYRIITEPTAAALAYGL 181
Oy 186 DTFKKEIRNVLIFEDLGGGTFEVSILTD--DS--IREVKAAGDHLGGEEDFQMLVNH 241
Db 182 QKAGDHTVYDILGGGTFEVSILTD--DS--IREVKAAGDHLGGEEDFQMLVNH 240
Oy 242 VEERKKEKKNIDISQKGFPEVDSVLEIEVDENQEPVIANNDQPSLEILOSPEID----FTSI 297
Db 241 VEERKKEKESINLKQDPLAQMLEAKPKATLESFOOTQVNLPVYAAAGSKFRLVAVY 300
Oy 298 TVAFREELQSDLRLETFEKAARDKADKQITHDVLVGSGRIPKVKLLDQFNRK 357
Db 301 SHAKLESIVEDLVQKTECFKAKDQALDVSQDILHEVLVQSGTMRKLVQNTVAERF--GK 359
Oy 358 DUNSLINDEAVAGAAVOALILMGDSKNNOYDILLDVAPLSLGLTACGATMLIKRNSIT 417
Db 360 EAKQDQVPEAVAGAIQGVYLSGD---VADVLLLVYPLTIGIELTIGCVATCLEKN 415
Oy 418 STPEIKQOIFETYSNDQPGVLTQVYEGEERANTKNNLLGRFELSGTPAPRGVYQVLEVP 477
Db 416 TPTPKASQVSTADDDQQAATJHVLVQSGKPMKNSKELNDITDTPAPMGHQPDLVETFDI 475
Oy 478 PIDANGILNVTATDQSGKANKTITINDKRSKEELTEMVQAKKKEDEVOERENAKN 537
Db 476 PIDANGILNVTASAKDQKQOSTVYKASG--LSEDEIQQVQDQVANAEDKKEFEELAA 534
Oy 538 ARNALESTAFNMKSAYDEGLAKRISDAKKVLDKQCYVISMULDANTLA--EKEDEEHR 596
Db 535 ARNAGQDLVATKAKKTEHAKGR--ATREKATIKER--ALGELEBAVAGDVALETKAK 588
Oy 597 KELOQVNPRIISGLY---GQAGGP 617
Db 589 NALQSAQSTPLQKQVABQAOQGEADP 614

* RESULT 11
US-09-759-010-1
; Sequence 1, Application US/09759010
; Patent No. US20010034042A1
; GENERAL INFORMATION:
; APPLICANT: Sitavatsa, Pramod K.
; TITLE OF INVENTION: COMPLEXES OF PEPTIDE BINDING FRAGMENTS OF HEAT-SHOCK
; TITLE OF INVENTION: PROTEINS AND THEIR USE AS IMMUNOTHERAPEUTIC AGENTS
; FILE REFERENCE: 8449-1135
; CURRENT FILING DATE: 2001-07-12
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ IDS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 637
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-010-1
Query Match 43.28: Score 1409; DB 10; Length 637;
Best Local Similarity 51.08; Pred No. 1, 5e-92;
Matches 314: Conservative 91; Mismatches 175; Indels 36; Gaps 14;
Oy 7 IDIDLITVYSCGVQFQHGVEIIANDQGNRTTSPSYAFT--DREHLIGDAANQVALLNPN 65
Db 4 IDIDLITVNSCVALLENGWVAVIEABACATTPSIIATYINDGEBTLVQGPABQAVATNPN 63
Oy 66 TVFAKRLIGKRGDPVQSGMKHMPQVYINQDQKRYQSYKGTATYFEELISSWLT 123
Db 64 TLFKRLIGKRGDPQDEVDQVIMFKRIIANDQGN---AMWEKQKQKKA--PQISAEV 118
Oy 124 LFKKKELEAVLGYPYNNVITVPAPFNSQKQATDQAGYAGLAVYRIITEPTAAALAY 183

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Db 119 LKMKKTAEDYLGEPTVAITVPAYFENDAQROTNRACRAGLGEYKRIINEPTAALAY 178
Oy 184 GIDRTGKGRNVNLIPTDLOGGTEDVSLITD--DG--TFEYVATADTHLGGEDENRVLVN 239
Db 179 GLDK-GGRKRTIAYVDGGSTFDSITLIEDVGEKTFEVLATNSDTHLGGEDDSRLIN 237
Oy 240 HPEYFPRKHKKXIOSKRNABRPLPACERAKRTLSSQASLEIDSLPFGI---DYT 235
Db 238 YLVEFFRKQOIGDIRDPLAMORLEKAEKAKTEISSLAQOQDVNLPITADTOPRKHNI 297
Oy 236 SITRAREELSGDLFRSTLEPEVERALBOKAKIDQIDHVLVGGSTRIPVOKLDDPFN 335
Db 298 KTRAKTLESLEVDLVNHSIEPLAKVADQBSVSDIDVILVGGOTRNPAPVOKKAVEFF- 356
Oy 356 GRLKMSINPDEAVAYGAOALITMGKSPNOYLLDLDAPLSLGLETAGVMTALIK 415
Db 357 GKPRKQVNPDEAVALGAAVOGVYNGD---VKDVLIDVYTPLSIGLETMGVMTTILA 412
Oy 416 RNSITPTKOTIPTYSDNQPVLIOYGEERAMTKDNMLGFEELSGETPAPRGVQITE 475
Db 413 KNTITPKNSQVYTAEDNSQASVATIHVQGRKRAKNSLQGMIDQINPAPRMPQOIE 472
Oy 476 VFEDIDANGILNVTATDQSPGKAKRTITTDNGRSLKEETIRBVOEAKYKAEDVORER 535
Db 473 VFEDIDANGILHVSARKDNGSKGKOTTKIKSSG-LNDEITOKRVADANAAEADRKFEEL 531
Oy 536 VSKNALESYAFPNKSAVEDDEGLGKISPAKRVKIDKOCQVYSIMDANTLAERD--- 591
Db 532 VOTNRQGDHLHASTRQVYERADK---LPADOKTAIE-----SALTALFTALGEOKAA 582
Oy 592 PEHRKRELDQVNCPTII 607
Db 583 IEAKMOELAOVSOKLM 598

```

RESULT 12
US-09-815-242-10015
Sequence 10015. Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel D.
APPLICANT: Cart, Grant J.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.01A US/09/815, 242
CURRENT FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/259,308
NUMBER OF SEQ ID NO: 10015
SOFTWARE: PASTSoc for Windows Version 4.0
SEQ ID NO: 10015
LENGTH: 638
TYPE: PRT
ORGANISM: Escherichia coli

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US-09-815-242-10015
Query March 43.2% Score 1409; DB 10; Length 638;
Best Local Similarity 51.0%; Pred. No. 1,5e-92;
Matches 314; Conservative 91; MismatchChgs -175; Indels 36; Gaps 14;
Oy 7 IIGDGLTTCYVADQGTTPRVLNMBGDRFTFSILATDQGETVLGQPKAKNOAVNPN 65
Db 5 IIGDGLTTCYVADQGTTPRVLNMBGDRFTFSILATDQGETVLGQPKAKNOAVNPN 64
Oy 66 TVDKAKLIGKREQDVQSDKMKMPQVIT--NDQDPFVQVYVSKGTETKAFPEELSSNV 123
Db 65 TLKAKELIGRRQDEVDQSDIMPKITADNDD---AVVEYKQKMA--PEQLSAEV 119
Oy 124 LTMRETAAYATGYPTNATYVAYFNDROGQATACQVATAGVATRIINPTAALAY 183
Db 120 LKMKKTAEDYLGEPTVAITVPAYFENDAQROTNRACRAGLGEYKRIINEPTAALAY 179
Oy 184 GIDRTGKGRNVNLIPTDLOGGTEDVSLITD--DG--TFEYVATADTHLGGEDENRVLVN 239
Db 180 GLDK-GGRKRTIAYVDGGSTFDSITLIEDVGEKTFEVLATNSDTHLGGEDDSRLIN 238
Oy 240 HPEYFPRKHKKXIOSKRNABRPLPACERAKRTLSSQASLEIDSLPFGI---DYT 235
Db 239 YLVEFFRKQOIGDIRDPLAMORLEKAEKAKTEISSLAQOQDVNLPITADTOPRKHNI 298
Oy 236 SITRAREELSGDLFRSTLEPEVERALBOKAKIDQIDHVLVGGSTRIPVOKLDDPFN 335
Db 299 KTRAKTLESLEVDLVNHSIEPLAKVADQBSVSDIDVILVGGOTRNPAPVOKKAVEFF- 357
Oy 356 GRLKMSINPDEAVAYGAOALITMGKSPNOYLLDLDAPLSLGLETAGVMTALIK 415
Db 358 GKPRKQVNPDEAVALGAAVOGVYNGD---VKDVLIDVYTPLSIGLETMGVMTTILA 413
Oy 416 RNSITPTKOTIPTYSDNQPVLIOYGEERAMTKDNMLGFEELSGETPAPRGVQITE 475
Db 414 KNTITPKNSQVYTAEDNSQASVATIHVQGRKRAKNSLQGMIDQINPAPRMPQOIE 473
Oy 476 VFEDIDANGILNVTATDQSPGKAKRTITTDNGRSLKEETIRBVOEAKYKAEDVORER 535
Db 474 VFEDIDANGILHVSARKDNGSKGKOTTKIKSSG-LNDEITOKRVADANAAEADRKFEEL 532
Oy 536 VSKNALESYAFPNKSAVEDDEGLGKISPAKRVKIDKOCQVYSIMDANTLAERD--- 591
Db 533 VOTNRQGDHLHASTRQVYERADK---LPADOKTAIE-----SALTALFTALGEOKAA 583
Oy 592 PEHRKRELDQVNCPTII 607
Db 584 IEAKMOELAOVSOKLM 599

```

RESULT 13
US-09-815-242-13713
Sequence 13713. Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel D.
APPLICANT: Cart, Grant J.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.01A US/09/815, 242
CURRENT FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/191,076
PRIOR APPLICATION NUMBER: 60/206,848

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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQUENCES: 4110
SOFTWARE: FASTED for Windows Version 4.0
SEQ ID NO 13713
LENGTH: 638
TYPE: PRT
ORGANISM: salmonella typhi
US-09-815-242-13713
Query Match
Best Local Similarity: 50.2%; Pred No 3,4e+32;
Matches 307; Conservative 95; Mismatches 183; Indels 26; Gaps 13;

Oy 7 1GIDLGTTSCVGVHGHGVVLIANDGQNTPTSPYAFDT-DT-ERLIGDMAANOVALLNPN 65
||||| ||||| : : : ||||| ||||| ||||| ||||| |||||
5 1GIDLGTTNSCAVIMDGTAVLENAEDBTPSTIATDQGTLLVQCPAARQATYNNON 64
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 66 TYPGAKRLIGKRCPPVGSOMKHPPOYINDGCKRKYVSKGRTKATYEEIISAVLT 125
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 65 TFLAKRLIGRRPOEDVROVSLMPTXIIIG-ADNGDAMLDYKQKKA--IPQISAKYK 121
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 126 KKKELIENALGYPTNNVITVPAPFNDGKQRTKAGYAGLNLVLRINERTPAALAVGL 185
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 122 KKKRTADYLGSEPTVAVITVPAPFNDGKQRTKAGLGLYKRLINERTPAALAVGL 181
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 186 DPTGCKERNVLTLDGGGFVFSVLTLD--DG--IEPKKATGDTHLGGEDPNRLNHF 241
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 182 DRE-VNRTIAYVDLGGTFPDISIEIDVDGDKETEVLLATNGDHLGGEDFPRLNVL 240
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 242 VEEKRRKHKNDISOKRAVRLRTACERAKRTLSSSTQASLEISLPEGID----PFTTSI 297
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 VEEKRKDQGLDNLNDPILAKRLEAKKATLSSAQDTVNLPTITADATGRHMINIV 300
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 288 TAAPEFELCSLPTSTLEPEYKALMDKPAIDKNOHOLVAGSPRIYKOKLLODFPNSG 357
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 TAAELSLVEDVANSIEPELVKALDQGLASVSDINVTIVGQFPMHPOKRAAEF-GK 359
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 358 DLAHSINPDEAVAGAAVOAAILMDGSKSENVODLLILVAPLSIGLETFAGCVTALIKRN 417
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 360 EBRKQDNPENAVAGAAVOAGVLTGSD--VADVLLDVTPLSLGIEITGCVMTPLIKR 415
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 418 STPTGQOIFPTYSNDQPGVLIQVGEGRAPFMDNNLGRRELSCGPPAPRGVPLEVTE 477
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 416 TPTTFHSQVSTADNDQPAVSIMVLGCEERKAAIDKSLGQFGLDGINAPRQMPOLEVT 475
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 478 FPDIAKCIUNVATDKSTGKANKITITINDGRLSKREELERNOVENEKYKADEVORENS 537
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 476 FPDIDQSLIHSKOKNSKSRGDKITITAKSSG--LMEERIOKRVDEENASDNRKEELVO 534
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 538 AANLALSYAFNMKSAYVEDGKLGKLSBANKKLVLDGCOVYSLMDANTALAR-KDEFEHR 596
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 535 TFGCGHLLHSTRKQVEANG--DKPLADDTAL----ESALSLELAKGEDKAAALEKK 588
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 597 KELEOVCPNPII 607
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 589 OELADVOVSQKLM 599
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||

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APPLICANT: Ohlsen, Karl L.
APPLICANT: Eysling, Judith W.
APPLICANT: Trivick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes In
E. COLI STRAIN K12
PRIOR APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQUENCES: 620
SOFTWARE: PDSBQ for Windows Version 4.0
SEQ ID NO 11472
LENGTH: 620
TYPE: PRT
ORGANISM: Helicobacter pylori
US-09-815-242-11472
Query Match
Best Local Similarity: 48.0%; Pred No 7,4e+32;
Matches 293; Conservative 115; Mismatches 172; Indels 30; Gaps 11;

Oy 7 1GIDLGTTSCVGVHGHGVVLIANDGQNTPTSPYAFDT-DT-ERLIGDMAANOVALLNPN 65
||||| ||||| : : : ||||| ||||| ||||| ||||| |||||
5 1GIDLGTTNSCAVIMDGTAVLENAEDBTPSTIATDQGTLLVQCPAARQATYNNON 64
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 66 TYPGAKRLIGKRCPPVGSOMKHPPOYINDGCKRKYVSKGRTKATYEEIISAVLT 125
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 65 TFLAKRLIGRRPOEDVROVSLMPTXIIIG-ADNGDAMLDYKQKKA--IPQISAKYK 121
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 126 KKKELIENALGYPTNNVITVPAPFNDGKQRTKAGYAGLNLVLRINERTPAALAVGL 185
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 122 KKKRTADYLGSEPTVAVITVPAPFNDGKQRTKAGLGLYKRLINERTPAALAVGL 181
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 186 DPTGCKERNVLTLDGGGFVFSVLTLD--DG--IEPKKATGDTHLGGEDPNRLNHF 241
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 182 DRE-VNRTIAYVDLGGTFPDISIEIDVDGDKETEVLLATNGDHLGGEDFPRLNVL 240
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 242 VEEKRRKHKNDISOKRAVRLRTACERAKRTLSSSTQASLEISLPEGID----PFTTSI 297
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 VEEKRKDQGLDNLNDPILAKRLEAKKATLSSAQDTVNLPTITADATGRHMINIV 300
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 288 TAAPEFELCSLPTSTLEPEYKALMDKPAIDKNOHOLVAGSPRIYKOKLLODFPNSG 357
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 TAAELSLVEDVANSIEPELVKALDQGLASVSDINVTIVGQFPMHPOKRAAEF-GK 359
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 358 DLAHSINPDEAVAGAAVOAAILMDGSKSENVODLLILVAPLSIGLETFAGCVTALIKRN 417
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 360 EBRKQDNPENAVAGAAVOAGVLTGSD--VADVLLDVTPLSLGIEITGCVMTPLIKR 415
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 418 STPTGQOIFPTYSNDQPGVLIQVGEGRAPFMDNNLGRRELSCGPPAPRGVPLEVTE 477
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 416 TPTTFHSQVSTADNDQPAVSIMVLGCEERKAAIDKSLGQFGLDGINAPRQMPOLEVT 475
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 478 FPDIAKCIUNVATDKSTGKANKITITINDGRLSKREELERNOVENEKYKADEVORENS 537
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 476 FPDIDQSLIHSKOKNSKSRGDKITITAKSSG--LMEERIOKRVDEENASDNRKEELVO 534
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 538 AANLALSYAFNMKSAYVEDGKLGKLSBANKKLVLDGCOVYSLMDANTALAR-KDEFEHR 596
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 535 TFGCGHLLHSTRKQVEANG--DKPLADDTAL----ESALSLELAKGEDKAAALEKK 588
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 597 KELEOVCPNPII 607
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 589 OELADVOVSQKLM 599
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GenCore version 5.1.3
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OK protein - protein search, using sw model

Run on: December 4, 2002, 16:41:27 : Search time 16 seconds
(Without alignments)
1178.756 Million cell updates/sec

Title: US-09-646-835-1

Sequence: 1263
1 MAAKAAAGIDGATGTCYGV.....FGAGCPKGGSSSGPTTEVD 641

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*

1: /cgn2.6/prodata/1/jaa/5A.COMB.pep.*
2: /cgn2.6/prodata/1/jaa/5B.COMB.pep.*
3: /cgn2.6/prodata/1/jaa/6A.COMB.pep.*
4: /cgn2.6/prodata/1/jaa/6B.COMB.pep.*
5: /cgn2.6/prodata/1/jaa/CTDS.COMB.pep.*
6: /cgn2.6/prodata/1/jaa/BackKiller1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2859.5	87.6	890	US-09-513-783A-174	Sequence 174, App
2	2856.5	87.6	646	US-08-441-139-14	Sequence 174, App
3	2717	83.0	643	US-08-797-358B-3	Sequence 3, Appl
4	2088.5	64.0	655	US-09-632-538C-36	Sequence 36, Appl
5	2032.5	62.9	666	US-08-441-139-16	Sequence 16, Appl
6	2001.5	62.6	653	US-08-441-139-11	Sequence 11, Appl
7	1950.5	55.8	679	US-08-441-119-5	Sequence 2, Appl
8	1897	58.1	663	US-08-441-139-7	Sequence 7, Appl
9	1897	58.1	663	US-08-214-583-2	Sequence 2, Appl
10	1476.5	45.2	679	US-08-441-139-4	Sequence 4, Appl
11	1438	44.1	641	US-09-066-047-5	Sequence 5, Appl
12	1375.5	44.0	649	US-09-134-001C-3646	Sequence 3646, App
13	1375.5	42.8	616	US-08-336-972-52	Sequence 52, Appl
14	1374	41.5	338	US-08-336-972-52	Sequence 52, Appl
15	1335	40.9	607	US-08-472-534-5	Sequence 5, Appl
16	1247.5	38.2	600	US-08-472-534-5	Sequence 5, Appl
17	985.5	30.2	315	US-08-227-073-7	Sequence 7, Appl
18	985.5	30.2	315	US-09-513-783A-172	Sequence 172, App
19	782	22.7	471	US-08-203-985B-14	Sequence 14, Appl
20	742	22.3	462	US-08-203-985B-14	Sequence 14, Appl
21	657.5	22.0	462	US-09-115-5813-1	Sequence 1, Appl
22	651.5	20.0	999	US-08-770-301A-1	Sequence 1, Appl
23	645.5	19.2	999	US-08-770-301A-1	Sequence 1, Appl
24	635.5	19.2	999	US-09-115-5813-1	Sequence 1, Appl
25	596.5	18.3	307	US-08-898-207A-481	Sequence 481, App
26	596.5	18.3	307	US-08-898-207A-481	Sequence 481, App
27	560.5	17.2	560	US-08-928-692-53	Sequence 53, Appl

ALIGNMENTS

28	560.5	17.2	560	US-09-339-972-53	Sequence 53, Appl
29	518	15.9	187	US-09-339-972-53	Sequence 53, Appl
30	454	13.9	374	US-08-328-692-51	Sequence 51, Appl
31	454	13.9	374	US-08-339-972-51	Sequence 51, Appl
32	445	13.6	168	US-08-441-139-10	Sequence 10, Appl
33	425	12.6	168	US-08-441-139-10	Sequence 10, Appl
34	326	12.6	559	US-05-060-983-9	Sequence 9, Appl
35	316	9.7	80	US-08-464-184-4	Sequence 4, Appl
36	316	9.7	80	US-08-338-057-4	Sequence 4, Appl
37	316	9.7	80	US-08-668-416-4	Sequence 4, Appl
38	286.5	8.8	77	US-08-553-7	Sequence 7, Appl
39	274.5	8.4	554	US-08-770-544-6	Sequence 6, Appl
40	274.5	8.4	554	US-08-770-544-6	Sequence 6, Appl
41	273.5	8.3	579	US-08-770-544-6	Sequence 6, Appl
42	254	7.8	183	US-09-556-877-301	Sequence 301, App
43	254	7.8	183	US-09-556-877-301	Sequence 301, App
44	254	7.8	183	US-09-420-412C-301	Sequence 301, App
45	248.5	7.6	136	US-09-183-861-49	Sequence 49, Appl

RESULT 1	US-09-513-783A-174	Sequence 174, Application US/09513783A
Patent No. 6416959		
GENERAL INFORMATION:		
APPLICANT:	Glaxo, Kenneth A.	
INVENTOR:	Glaxo, Kenneth A.	
TITLE REFERENCE:	97-022-11	
FILE REFERENCE:	97-022-11	
CURRENT APPLICATION NUMBER:	US/09513783A	
NUMBER OF SEQ ID NOS:	180	
SOFTWARE:	Patent Ver. 2.0	
SEQ ID NO:	180	
SEQ ID NO:	180	
ORGANISM:	Artificial Sequence	
FEATURE:		
OTHER INFORMATION:	Description of Artificial Sequence: GFP-HSC70	
US-09-513-783A-174		
Query Match	87.6%	Score 2859.5, DB 4, Length 890.
Similarity	85.6%	Score 2856.5, DB 2, Length 646.
Matches 553:	Conservative 48:	Mismatches 40:
		Indels 5:
		Gaps 3:
QY	1	MAKAAAGIDGATGTCYGVFOHKKVEIINADGGRFTTSVAFDTGRIIDAAKNQYA 60
DB	245	MSGGAVGIDGATGTCYGVFOHKKVEIINADGGRFTTSVAFDTGRIIDAAKNQYA 304
QY	61	MPETVFAKRLIGRRDAVQDSQKMPFVYNDGCKRQVYSGYKGAATYEEIS 120
DB	305	MPETVFAKRLIGRRDAVQDSQKMPFVYNDGCKRQVYSGYKGAATYEEIS 120
QY	121	SVTLFRKKEIAEAVLGVTNVTTPAFAFDSQSGTAGVAGIAGLVLRINEPTAA 180
DB	365	SVTLFRKKEIAEAVLGVTNVTTPAFAFDSQSGTAGVAGIAGLVLRINEPTAA 180
QY	181	IANGDKRKEKRNVLFDGSGGTFVSLTIDGIFEXKSNADTFHGGEDFONRNH 240
DB	425	IANGDKRKEKRNVLFDGSGGTFVSLTIDGIFEXKSNADTFHGGEDFONRNH 240
QY	241	FVEERFKRKNDISQKFAVRRLTCEBAKRLSSSTASLEIUSLFEDIGFTYSITRA 300
DB	485	FVEERFKRKNDISQKFAVRRLTCEBAKRLSSSTASLEIUSLFEDIGFTYSITRA 300
QY	301	PIERKRCRKRKDKSEKRAFRKLRKAGKATLSSSTASLEIUSLFEDIGFTYSITRA 360
DB	545	PIERKRCRKRKDKSEKRAFRKLRKAGKATLSSSTASLEIUSLFEDIGFTYSITRA 360
QY	361	KSINDEKVAAGAAVQAAIIMDKSERVODLLILVAPLSIGLEPAGVFAIKRNSFI 420

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Db 605 KSINDEBAVAGAAVOAALIMGSKSNVODILLDVLPLSLGLETAGVATVLIKNRTT 664
Qy 421 PPKGQIIFFTTSNDQPVLLQVYEEGERAMTKNNLLGFEELSGIPAPRGVPIEVTPI 480
Db 665 PPKGQIIFFTTSNDQPVLLQVYEEGERAMTKNNLLGFEELSGIPAPRGVPIEVTPI 724
Qy 481 DANGILAVTNDKSGKANKITITNKGRLSEETREBVOARVKAEDEVOERYSARK 540
Db 725 DANGILAVTNDKSGKANKITITNKGRLSEETREBVOARVKAEDEVOERYSARK 784
Qy 541 ALESYAFNMKSAVEDGLGKISEADKKYVLDKCOEIVSMILANTLAKOEFEHKKKELE 600
Db 785 SLESYAFNMKSAVEDGLGKISEADKKYVLDKCOEIVSMILANTLAKOEFEHKKKELE 844
Qy 601 QVCPNITSLYOGAGG--PG--GAGCGKSGSGPTTIEVD 641
Db 845 KVCNPIITKLYSGAGMFGMGPGFGAGAPSGGASGPTTIEVD 890

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RESULT 2

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US-08-441-139-14
Sequence 14, Application US/08441139
Patent No. 5773245

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GENERAL INFORMATION:
APPLICANT: Millrup, Dr. Karl D.
INVENTOR: Millrup, Dr. Karl D., James S. FOR IMPROVING SECRETION OF
TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
STATE: NY
COUNTRY: USA
ZIP: 11530

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441.139
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,997
INVENTOR: SCULLY, SCOTT, MURPHY & PRESSER
ATTORNEY/AGENT INFORMATION:
NAME: DIGDILL, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8646
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
FAX: 516-742-4366
TEXT: 516-742-4366
SEQUENCE CHARACTERISTICS:
LENGTH: 646 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-441-139-14

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Query Match

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Best Local Similarity 87.5%: Score 2856.5: DB 1: Length 646:
Matches 553: Conservative 47: Mismatches 41: Indels 5: Gaps 3:

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Qy 1 MAKAALIGDITGYSCVGVQGRKVELIANDQGNRTTSPYVAFPTRELIGDAKKNOYA 60
Db 1 MKNPANGISDGLTTSQVGVQGRKVELIANDQGNRTTSPYVAFPTRELIGDAKKNOYA 60

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Qy 61 LPNQKTFDAKRLIGRKFEDPVVQSGMHPPOVITIDGDKPKYQVSGKGTAKYPEETS 120
Db 61 MNPNTVFPDAKRLIGRKFEDAVVQSGMHPPOVITIDGDKPKYQVSGKGTAKYPEETS 120
Qy 121 SVALTKKEINAVLGYPVYANAVTPVAVPNDGQKATKAGVYAGLANTLINSPTAA 180
Db 121 SVALTKKEINAVLGYPVYANAVTPVAVPNDGQKATKAGVYAGLANTLINSPTAA 180
Qy 181 IAVGIDRGKGEENLVLFPLGSGTGPVSYITLIDGCFYVAPADGTHLGGEDPRKYN 240
Db 181 IAVGIDRGKGEENLVLFPLGSGTGPVSYITLIDGCFYVAPADGTHLGGEDPRKYN 240
Qy 241 PVEETKRAKKKDIQNSRAVRLRLTACERAKTPTLSSSTQSLTIDSLPGIDETYSITTA 300
Db 241 PVEETKRAKKKDIQNSRAVRLRLTACERAKTPTLSSSTQSLTIDSLPGIDETYSITTA 300
Qy 301 RFELCSDFPSTLPEVERALPAKDKACHIDLYVAGSGTNPVPOVXKLDDFPNGDAN 360
Db 301 RFELCSDFPSTLPEVERALPAKDKACHIDLYVAGSGTNPVPOVXKLDDFPNGDAN 360
Qy 361 KSINDEBAVAGAAVOAALIMGSKSNVODILLDVLPLSLGLETAGVATVLIKNRTT 420
Db 361 KSINDEBAVAGAAVOAALIMGSKSNVODILLDVLPLSLGLETAGVATVLIKNRTT 420
Qy 421 PPKGQIIFFTTSNDQPVLLQVYEEGERAMTKNNLLGFEELSGIPAPRGVPIEVTPI 480
Db 421 PPKGQIIFFTTSNDQPVLLQVYEEGERAMTKNNLLGFEELSGIPAPRGVPIEVTPI 480
Qy 481 DANGILAVTNDKSGKANKITITNKGRLSEETREBVOARVKAEDEVOERYSARK 540
Db 481 DANGILAVTNDKSGKANKITITNKGRLSEETREBVOARVKAEDEVOERYSARK 540
Qy 541 ALESYAFNMKSAVEDGLGKISEADKKYVLDKCOEIVSMILANTLAKOEFEHKKKELE 600
Db 541 SLESYAFNMKSAVEDGLGKISEADKKYVLDKCOEIVSMILANTLAKOEFEHKKKELE 600
Qy 601 QVCPNITSLYOGAGG--PG--GAGCGKSGSGPTTIEVD 641
Db 601 KVCNPIITKLYSGAGMFGMGPGFGAGAPSGGASGPTTIEVD 646

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RESULT 3

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US-08-797-3589-3
Sequence 3, Application US/087973589
Patent No. 6564728

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GENERAL INFORMATION:
APPLICANT: Adams, John
INVENTOR: INTAFCELLULAR VITAMIN D BINDING PROTEIN
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Plotes LLP
STREET: 300 Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797.3589
FILING DATE: 11-Feb-1997
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA: US 60/011,491
FILING DATE: 12-FEB-1995

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ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CE 3165
TELECOMMUNICATION INFORMATION:

```


: TELEPHONE: (619) 535-9001
 : TELEFAX: (619) 535-8949
 : INFORMATION FOR SEQ ID NO: 3:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 643 amino acids
 : STRAND: single
 : TOPOLOGY: unknown
 : MOLECULE TYPE: protein
 : SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-08-797-358B-3

Query Match

Query Similarity 83.38; Score 2717; DB 4; Length 643;
 Matched 519; Conservative 62; Mismatches 55; Indels 0; Gaps 0;

QY 6 A I D I G T T T S C V G F O R K V E I I A N D G N R T P S V A F T D E R I G D A N K A N G V A L N P O N T 65
 D B A I D I G T T T S C V G F O R K V E I I A N D G N R T P S V A F T D E R I G D A N K A N G V A L N P O N T 67
 QY 8 A V I D A L L T T S C V G F O R K V E I I A N D G N R T P S V A F T D E R I G D A N K A N G V A L N P O N T 67
 D B A V I D A L L T T S C V G F O R K V E I I A N D G N R T P S V A F T D E R I G D A N K A N G V A L N P O N T 125
 QY 66 T V D A N L I G R K R P A V Y O A M K K H P P O Y I N D G A P P V O S Y K G T A K A F P E E L S A M V T 125
 D B T V D A N L I G R K R P A V Y O A M K K H P P O Y I N D G A P P V O S Y K G T A K A F P E E L S A M V T 127
 QY 126 K M E I A E A V I G P V T N A V I T V A F N D S O R A T K D A G V A G I A N V A I I N E P T A A I A N G L 185
 D B K M E I A E A V I G P V T N A V I T V A F N D S O R A T K D A G V A G I A N V A I I N E P T A A I A N G L 187
 QY 128 K M E I A E A V I G P V K H A V I T V A F N D S O R A T K D A G V A G I A N V A I I N E P T A A I A N G L 187
 D B K M E I A E A V I G P V K H A V I T V A F N D S O R A T K D A G V A G I A N V A I I N E P T A A I A N G L 245
 QY 186 D R G G R R N V I I P L D G G T F D V S I T I D I G I P E K A N K R L I S S T O A S L E I D L P E G I D Y T S I T R A F E E L 245
 D B D R G G R R N V I I P L D G G T F D V S I T I D I G I P E K A N K R L I S S T O A S L E I D L P E G I D Y T S I T R A F E E L 247
 QY 246 K R H K K D I S O N K R A V R L R T A C E A R K R L I S S T O A S L E I D L P E G I D Y T S I T R A F E E L 305
 D B K R H K K D I S O N K R A V R L R T A C E A R K R L I S S T O A S L E I D L P E G I D Y T S I T R A F E E L 307
 QY 248 R R H K K D I S O N K R A V R L R T A C E A R K R L I S S T O A S L E I D L P E G I D Y T S I T R A F E E L 307
 D B R R H K K D I S O N K R A V R L R T A C E A R K R L I S S T O A S L E I D L P E G I D Y T S I T R A F E E L 365
 QY 306 C S D L P E R T L E P Y E K A L D A K L O K I H D V Y G S T R I P R V O K L I D O F F N G D A N K S I N P 365
 D B C S D L P E R T L E P Y E K A L D A K L O K I H D V Y G S T R I P R V O K L I D O F F N G D A N K S I N P 367
 QY 366 D E A V A G A V A O A I M G K S E N V O D L L I D V A F L S L E T A G V M T A L I R N S T I P K O T 425
 D B D E A V A G A V A O A I M G K S E N V O D L L I D V A F L S L E T A G V M T A L I R N S T I P K O T 427
 QY 368 D E A V A G A V A O A I M G K S E N V O D L L I D V A F L S L E T A G V M T A L I R N S T I P K O T 427
 D B D E A V A G A V A O A I M G K S E N V O D L L I D V A F L S L E T A G V M T A L I R N S T I P K O T 485
 QY 426 Q I T T Y S D N O P G V I O Y E G E R A M T K D N N L G F E L S G I P P A P R G V P O I E V T F I D A N G I 485
 D B Q I T T Y S D N O P G V I O Y E G E R A M T K D N N L G F E L S G I P P A P R G V P O I E V T F I D A N G I 487
 QY 428 Q I T T Y S D N O P G V I O Y E G E R A M T K D N N L G F E L S G I P P A P R G V P O I E V T F I D A N G I 487
 D B Q I T T Y S D N O P G V I O Y E G E R A M T K D N N L G F E L S G I P P A P R G V P O I E V T F I D A N G I 545
 QY 486 L A N T A D K S T G A N K I T T I N D G R L S K E R I F R V O D E A K Y A E D V O K E A N A L E S Y 545
 D B L A N T A D K S T G A N K I T T I N D G R L S K E R I F R V O D E A K Y A E D V O K E A N A L E S Y 547
 QY 488 L A N T A D K S T G A N K I T T I N D G R L S K E R I F R V O D E A K Y A E D V O K E A N A L E S Y 547
 D B L A N T A D K S T G A N K I T T I N D G R L S K E R I F R V O D E A K Y A E D V O K E A N A L E S Y 605
 QY 546 A P M K A S A V E D G L G K R I T T E A D K R V I L D K O C E V I S N L D A N T A K R P E R K R E L E D V C N 605
 D B A P M K A S A V E D G L G K R I T T E A D K R V I L D K O C E V I S N L D A N T A K R P E R K R E L E D V C N 607
 QY 548 V F V F V G S L O E S L A N D I K R E D R H V O D K O R P A L T E H N O L A D K E R Y H O K R E L E Q I C R P 607
 D B V F V F V G S L O E S L A N D I K R E D R H V O D K O R P A L T E H N O L A D K E R Y H O K R E L E Q I C R P 641
 QY 606 I I S G L Y O G A G P G P G F G A G C G S G S G C P T I E E V D 641
 D B I I S G L Y O G A G P G P G F G A G C G S G S G C P T I E E V D 643
 QY 608 I I S R L I G G F G V Y G G S S C O A N Q D M S T O P L I E E V D 643
 D B I I S R L I G G F G V Y G G S S C O A N Q D M S T O P L I E E V D 643

RESULT 4

US-09-632-538C-36
 : Sequence 36, Application US/09632538C
 : Patent No. 6440674
 : GENERAL INFORMATION:
 : APPLICANT: Santos et al.
 : TITLE OF INVENTION: PHOSPHOR DERIVED FROM LUMINAL BINDING PROTEIN GENE AND METHOD
 : TITLE OF INVENTION: ITS USE
 : FILE REFERENCE: 54359
 : CURRENT APPLICATION NUMBER: US/09/632,538C
 : CURRENT FILING DATE: 2000-08-04
 : NUMBER OF SEQ ID NOS: 37

: SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 36
 : LENGTH: 655
 : TYPE: PRT
 : ORGANISM: Pseudotsuga menziesii
 US-09-632-538C-36

Query Match

Query Similarity 64.08; Score 2088.5; DB 4; Length 655;
 Best Local Similarity 65.28; Pred. No. 3,5e-162;
 Matches 402; Conservative 98; Mismatches 114; Indels 3; Gaps 3;

QY 7 I G I D I G T T T S C V G F O R K V E I I A N D G N R T P S V A F T D E R I G D A N K A N G V A L N P O N T 66
 D B I G I D I G T T T S C V G F O R K V E I I A N D G N R T P S V A F T D E R I G D A N K A N G V A L N P O N T 88
 QY 29 I G I D I G T T T S C V G F O R K V E I I A N D G N R T P S V A F T D E R I G D A N K A N G V A L N P O N T 88
 D B I G I D I G T T T S C V G F O R K V E I I A N D G N R T P S V A F T D E R I G D A N K A N G V A L N P O N T 125
 QY 67 V F P A R K L I G R K R P A V Y O A M K K H P P O Y I N D G A P P V O S Y K G T A K A F P E E L S A M V T 125
 D B V F P A R K L I G R K R P A V Y O A M K K H P P O Y I N D G A P P V O S Y K G T A K A F P E E L S A M V T 148
 QY 68 V F V F V G S L O E S L A N D I K R E D R H V O D K O R P A L T E H N O L A D K E R Y H O K R E L E Q I C R P 148
 D B V F V F V G S L O E S L A N D I K R E D R H V O D K O R P A L T E H N O L A D K E R Y H O K R E L E Q I C R P 185
 QY 126 K M E I A E A V I G P V T N A V I T V A F N D S O R A T K D A G V A G I A N V A I I N E P T A A I A N G L 185
 D B K M E I A E A V I G P V T N A V I T V A F N D S O R A T K D A G V A G I A N V A I I N E P T A A I A N G L 208
 QY 149 K M E I A E A V I G P V K H A V I T V A F N D S O R A T K D A G V A G I A N V A I I N E P T A A I A N G L 208
 D B K M E I A E A V I G P V K H A V I T V A F N D S O R A T K D A G V A G I A N V A I I N E P T A A I A N G L 245
 QY 186 D R G G R R N V I I P L D G G T F D V S I T I D I G I P E K A N K R L I S S T O A S L E I D L P E G I D Y T S I T R A F E E L 245
 D B D R G G R R N V I I P L D G G T F D V S I T I D I G I P E K A N K R L I S S T O A S L E I D L P E G I D Y T S I T R A F E E L 267
 QY 209 D R G G - G E K N I L V D G G T F D V S I T I D I G V F V S L S D H I L G G E D F D R M O Y E F K I V 267
 D B D R G G - G E K N I L V D G G T F D V S I T I D I G V F V S L S D H I L G G E D F D R M O Y E F K I V 305
 QY 246 K R H K K D I S O N K R A V R L R T A C E A R K R L I S S T O A S L E I D L P E G I D Y T S I T R A F E E L 305
 D B K R H K K D I S O N K R A V R L R T A C E A R K R L I S S T O A S L E I D L P E G I D Y T S I T R A F E E L 327
 QY 266 K R H K K D I S O N K R A V R L R T A C E A R K R L I S S T O A S L E I D L P E G I D Y T S I T R A F E E L 327
 D B K R H K K D I S O N K R A V R L R T A C E A R K R L I S S T O A S L E I D L P E G I D Y T S I T R A F E E L 365
 QY 306 C S D L P E R T L E P Y E K A L D A K L O K I H D V Y G S T R I P R V O K L I D O F F N G D A N K S I N P 365
 D B C S D L P E R T L E P Y E K A L D A K L O K I H D V Y G S T R I P R V O K L I D O F F N G D A N K S I N P 447
 QY 328 N M D L F K K T L G P Y K A L D A N L D K E I N E I V D G S T R I F R V O D L L K D L F G C E R N G V N P 387
 D B N M D L F K K T L G P Y K A L D A N L D K E I N E I V D G S T R I F R V O D L L K D L F G C E R N G V N P 425
 QY 366 D E A V A G A V A O A I M G K S E N V O D L L I D V A F L S L E T A G V M T A L I R N S T I P K O T 425
 D B D E A V A G A V A O A I M G K S E N V O D L L I D V A F L S L E T A G V M T A L I R N S T I P K O T 447
 QY 368 D E A V A G A V A O A I M G K S E N V O D L L I D V A F L S L E T A G V M T A L I R N S T I P K O T 447
 D B D E A V A G A V A O A I M G K S E N V O D L L I D V A F L S L E T A G V M T A L I R N S T I P K O T 485
 QY 426 Q I T T Y S D N O P G V I O Y E G E R A M T K D N N L G F E L S G I P P A P R G V P O I E V T F I D A N G I 485
 D B Q I T T Y S D N O P G V I O Y E G E R A M T K D N N L G F E L S G I P P A P R G V P O I E V T F I D A N G I 507
 QY 448 Q I T T Y S D N O P G V I O Y E G E R A M T K D N N L G F E L S G I P P A P R G V P O I E V T F I D A N G I 507
 D B Q I T T Y S D N O P G V I O Y E G E R A M T K D N N L G F E L S G I P P A P R G V P O I E V T F I D A N G I 545
 QY 486 L A N T A D K S T G A N K I T T I N D G R L S K E R I F R V O D E A K Y A E D V O K E A N A L E S Y 545
 D B L A N T A D K S T G A N K I T T I N D G R L S K E R I F R V O D E A K Y A E D V O K E A N A L E S Y 567
 QY 508 L A N T A D K S T G A N K I T T I N D G R L S K E R I F R V O D E A K Y A E D V O K E A N A L E S Y 567
 D B L A N T A D K S T G A N K I T T I N D G R L S K E R I F R V O D E A K Y A E D V O K E A N A L E S Y 604
 QY 546 A P M K A S A V - E D G L G K R I S A D K R V I L D K O C E V I S N L D A N T A K R P E R K R E L E D V C N 604
 D B A P M K A S A V - E D G L G K R I S A D K R V I L D K O C E V I S N L D A N T A K R P E R K R E L E D V C N 627
 QY 548 V Y M K S T I N E K D I A D K R I D E B K R E I T A I E A L E M L D N O S A K E D P E R K L E V A V S 627
 D B V Y M K S T I N E K D I A D K R I D E B K R E I T A I E A L E M L D N O S A K E D P E R K L E V A V S 644
 QY 605 I I S G L Y O G A G P G P G 621
 D B I I S G L Y O G A G P G P G 644

RESULT 5

US-08-441-139-16
 : Sequence 16, Application US/08441139
 : Patent No. 675853
 : GENERAL INFORMATION:
 : APPLICANT: Wiltup, Dr. Karl D.
 : APPLICANT: Robinson, Anne S.
 : TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
 : TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
 : NUMBER OF SEQUENCES: 20
 : CORRESPONDENCE ADDRESS: MORT MURPHY & PRESSER
 : STREET: 400 Garden City Plaza
 : CITY: Garden City
 : STATE: NY
 : COUNTRY: USA
 : ZIP: 11530

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,139
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: US 08/089,997
PRIORITY APPLICATION DATE: 1993
ATTORNEY/AGENT INFORMATION:
NAME: DIGITAL, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8646
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 240 901 5454
TELEX: 240 901 5454
INFORMATION FOR SEQ. ID NO.: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 666 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-441-139-16

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Query Match 62.9%, Score 2052.5; DB 1; Length 666;
Best Local Similarity 64.7%; Pred. No. 3,1e-159;
Matches 400; Conservative 105; Mismatches 106; Indels 7; Gaps 6;

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Oy 7 IGIDLTTCVGVYVNGKVEITLNDGQNTTPSYVAFT-DTERLIGDAKNOVYALNPN 65
Db 43 VQIDLTTCVGVYVNGKVEITLNDGQNTTPSYVAFTPEGRLIGDAKNOVYALNPN 102
Oy 66 TVYFAKRLIGRKRGDPVYVSGDKHMPQVINDGKPKVQVSY-KGRTKAFPEETISMWL 124
Db 103 TVYFAKRLIGRKRGDPVYVSGDKHMPQVINDGKPKVQVSY-KGRTKAFPEETISMWL 162
Oy 125 TVYFAKRLIGRKRGDPVYVSGDKHMPQVINDGKPKVQVSY-KGRTKAFPEETISMWL 184
Db 163 TVYFAKRLIGRKRGDPVYVSGDKHMPQVINDGKPKVQVSY-KGRTKAFPEETISMWL 222
Oy 185 LDRGKGERNNLIFPDGSGTGVSYILITIDGQIFPVANAGDTHLGSDPDNRKLVNHPVEE 244
Db 223 LDRK-EGEKNLIFPDGSGTGVSYILITIDGQIFPVANAGDTHLGSDPDNRKLVNHPVEE 281
Oy 245 FRKHKKDTSQNRKAVRRLPACERAKRTSSQASLETDSLFGCIDYTSITTAARPEE 304
Db 282 YKRTKGVDNRKAVRRLPACERAKRTSSQASLETDSLFGCIDYTSITTAARPEE 341
Oy 305 LGSDFRSTLEPVEKALRLAKDKQAIDVLYVVGSGSTRIPVQKLLDFFNGRDLNKNIS 364
Db 342 LMDRLFRSTLEPVEKALRLAKDKQAIDVLYVVGSGSTRIPVQKLLDFFNGRDLNKNIS 401
Oy 365 PDEAVYGAAYOALITMGSKXNDIDELVAVLSGSTRIPVQKLLDFFNGRDLNKNIS 424
Db 402 PDEAVYGAAYOALITMGSKXNDIDELVAVLSGSTRIPVQKLLDFFNGRDLNKNIS 459
Oy 425 TQITFTYSNDQPROVLIQVTEGSRAMKDNMLGSEFELSGIPEAPVPGVQILEVFDIDMNG 484
Db 460 TQITFTYSNDQPROVLIQVTEGSRAMKDNMLGSEFELSGIPEAPVPGVQILEVFDIDMNG 519
Oy 485 ILNVTATQKSGKANKTTIDNGRGLSPEETIRWQOAEAYKADPOGESEYKAKMALS 544
Db 520 ILNVTATQKSGKANKTTIDNGRGLSPEETIRWQOAEAYKADPOGESEYKAKMALS 579
Oy 545 YVFMKASVED-EGUKGKRLSEAKKKVYLDQCEVYSMDAHLTAKEPEIKERKLELDVQ 603
Db 580 YVFMKASVED-EGUKGKRLSEAKKKVYLDQCEVYSMDAHLTAKEPEIKERKLELDVQ 639

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Oy 604 NPILISLYGACAGCPGPG 621
Db 640 QPVSUKLY-GSAGPEPTG 656

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RESULT 6
US-08-441-139-11
Sequence 11, Application US/08/441139
Patent No. 5773245

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GENERAL INFORMATION:
APPLICANT: WATSON, DR. Karl D.
TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
TITLE OR INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESS: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
STATE: Garden City
COUNTRY: USA
ZIP: 11530

```

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,139
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: US 08/089,997
PRIORITY APPLICATION DATE: 1993
ATTORNEY/AGENT INFORMATION:
NAME: DIGITAL, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8646
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 240 901 5454
TELEX: 240 901 5454
INFORMATION FOR SEQ. ID NO.: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 654 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-441-139-11

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Query Match 62.6%, Score 2042.5; DB 1; Length 654;
Best Local Similarity 64.6%; Pred. No. 2e-158;
Matches 399; Conservative 104; Mismatches 108; Indels 7; Gaps 6;

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Oy 7 IGIDLTTCVGVYVNGKVEITLNDGQNTTPSYVAFT-DTERLIGDAKNOVYALNPN 65
Db 31 VQIDLTTCVGVYVNGKVEITLNDGQNTTPSYVAFTPEGRLIGDAKNOVYALNPN 90
Oy 66 TVYFAKRLIGRKRGDPVYVSGDKHMPQVINDGKPKVQVSY-KGRTKAFPEETISMWL 124
Db 103 TVYFAKRLIGRKRGDPVYVSGDKHMPQVINDGKPKVQVSY-KGRTKAFPEETISMWL 162
Oy 125 TVYFAKRLIGRKRGDPVYVSGDKHMPQVINDGKPKVQVSY-KGRTKAFPEETISMWL 184
Db 163 TVYFAKRLIGRKRGDPVYVSGDKHMPQVINDGKPKVQVSY-KGRTKAFPEETISMWL 222
Oy 185 LDRGKGERNNLIFPDGSGTGVSYILITIDGQIFPVANAGDTHLGSDPDNRKLVNHPVEE 244
Db 223 LDRK-EGEKNLIFPDGSGTGVSYILITIDGQIFPVANAGDTHLGSDPDNRKLVNHPVEE 281
Oy 245 FRKHKKDTSQNRKAVRRLPACERAKRTSSQASLETDSLFGCIDYTSITTAARPEE 304
Db 282 YKRTKGVDNRKAVRRLPACERAKRTSSQASLETDSLFGCIDYTSITTAARPEE 341
Oy 305 LGSDFRSTLEPVEKALRLAKDKQAIDVLYVVGSGSTRIPVQKLLDFFNGRDLNKNIS 364
Db 342 LMDRLFRSTLEPVEKALRLAKDKQAIDVLYVVGSGSTRIPVQKLLDFFNGRDLNKNIS 401
Oy 365 PDEAVYGAAYOALITMGSKXNDIDELVAVLSGSTRIPVQKLLDFFNGRDLNKNIS 424
Db 402 PDEAVYGAAYOALITMGSKXNDIDELVAVLSGSTRIPVQKLLDFFNGRDLNKNIS 459
Oy 425 TQITFTYSNDQPROVLIQVTEGSRAMKDNMLGSEFELSGIPEAPVPGVQILEVFDIDMNG 484
Db 460 TQITFTYSNDQPROVLIQVTEGSRAMKDNMLGSEFELSGIPEAPVPGVQILEVFDIDMNG 519
Oy 485 ILNVTATQKSGKANKTTIDNGRGLSPEETIRWQOAEAYKADPOGESEYKAKMALS 544
Db 520 ILNVTATQKSGKANKTTIDNGRGLSPEETIRWQOAEAYKADPOGESEYKAKMALS 579
Oy 545 YVFMKASVED-EGUKGKRLSEAKKKVYLDQCEVYSMDAHLTAKEPEIKERKLELDVQ 603
Db 580 YVFMKASVED-EGUKGKRLSEAKKKVYLDQCEVYSMDAHLTAKEPEIKERKLELDVQ 639

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Db 270 YKKKCGDKVRKONRAVOKLREVEKAKRALSOSHQARLEISPFEGEDFSFTLRKAPFE 329
 QY 305 LCSDFSTLEPVEKALBDKAKDIAOHDIYVGGSTRIPKQKLLDGFNDRLOLKNIN 364
 Db 330 LNMDFJSTKMPKVKVLEDSOLKSDLDIEVLVGGSTRIPKLDQWKEFNKSPKSGIN 389
 QY 365 PDPAVAAVGAOAILMGDKSENVDLLIDVAPLSLGLETFAGVFWALIKNSTIPKQ 424
 Db 390 PDPAVAAVGAOAVGLSD -ODTGDIYLDVCPLLGLGLETFVGGVFKLIPRNVPTK 447
 QY 425 TQFTFYSONDQGVLYQVYEGERAKMDNLTGRELSGIPAPARGVQJEVTFDIDANG 484
 Db 448 SQTSTFASNDQPVTVYVYEGERPLTKDNHILDTGLGIPAPARGVQJEVTFDIDANG 507
 QY 489 ILWVATDSTGKANKTITNDKGRSKETIEBKVQAKKXKADQVOREVSANALBSYA 544
 Db 508 ILWVATDSTGSKNNKITNDKGRSKETIEBKVQAKKXKADQVOREVSANALBSYA 567
 QY 545 YAKNKSAVED-BGLKNGKISEADKKRYLDKCOEYISMLDAPTLAKDEPFHKRELEJOYC 603
 Db 566 YAKNKSAVED-BGLKNGKISEADKKRYLDKCOEYISMLDAPTLAKDEPFHKRELEJOYC 621
 QY 604 YAKNKSAVED-BGLKNGKISEADKKRYLDKCOEYISMLDAPTLAKDEPFHKRELEJOYC 621
 Db 628 OPTISIKLY-GSAGPEPTG 644

RESULT 7
 US-08-441-139-2
 / Sequence 2, Application US/08441139
 / Patent No. 5773245
 / GENERAL INFORMATION:
 / APPLICANT: Wiltup, Dr. Karl D.
 / APPLICANT: Robinson, Anne S.
 / TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
 / PROTEIN IN BACTERIA
 / TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
 / NUMBER OF SEQUENCES: 20
 / CORRESPONDENCE ADDRESS:
 / ADDRESS: SCULLY, SCOTT, MURPHY & PRESSER
 / STREET: 400 Garden City Plaza
 / CITY: Garden City
 / STATE: NY
 / COUNTRY: USA
 / ZIP: 11530
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/441,139
 / FILING DATE: 15-MAY-1995
 / PRIORITY APPLICATION DATA:
 / PRIORITY APPLICATION NUMBER: US 08/089,997
 / FILING DATE: 06-JUL-1993
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Digilio, Frank S.
 / REGISTRATION NUMBER: 31,346
 / ADDRESS: SCULLY, SCOTT, MURPHY & PRESSER
 / TELEPHONE: 516-742-4343
 / TELEFAX: 516-742-4366
 / TELEX: 230 901 SANS UR
 / INFORMATION FOR SEQ ID NO: 2:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 682 amino acids
 / TOPOLOGY: linear
 / MOLECULE TYPE: Protein
 / US-08-441-139-2

Best Local Similarity 62.9%; Pred. No. 4, Re-125;
 Matches 388; Conservative 102; Mismatches 155; Indels 5; Gaps 4;

QY 7 IGDIDCTTSCYGVFOHOKVEILINDQGRFTTSSVAFVDEIRLIGDAAKNOVALMPONT 66
 Db 53 IGDIDCTTSCYGVFOHOKVEILINDQGRFTTSSVAFVDEIRLIGDAAKNOVALMPONT 112
 QY 67 VFAKALIGKRGDPVYQVQSMKMRPQVINDQKRYKQVQKTRKAPYERISNWLTK 126
 Db 113 IFPIRKLIGLAKNRQVOKRKHLPFWVNMOKDAVEVSKQKGVFPFERISQMLTK 172
 QY 127 MKSILNAVLYGVYVNAVTVPAVFNQSORATKQVYAGLVARTIINEPTAAIATGSD 186
 Db 173 MKQIADYLGTVHAYVAFVAFVAFVAFVAFVAFVAFVAFVAFVAFVAFVAFVAFV 232
 QY 187 KTKEDNRYLFDLGGFPVYVAFVAFVAFVAFVAFVAFVAFVAFVAFVAFVAFVAFV 246
 Db 233 KSKK-EHQIIVYDGGGFFVSLISLNQVEVQATSDHLSGDEPPIYVIRLOLIRAK 291
 QY 247 RKHKNDISOKRAVRLTQCEKAKRTSSVTAQSLDEISLREQIDVFTSTIRARPELC 306
 Db 292 KKHGIDVSDNNKALAKRAENAKRALSQSKSTREIDSDPQDIDSLSTIRAKPELIN 351
 QY 307 SDFSTLEPVEKALBDKAKDIAOHDIYVGGSTRIPKQKLLDGFNDRLOLKNIN 366
 Db 352 LDFKRTKPKVEKYLQDSGLEKKDDVDIYVCGSTRIPKQVLLSEYDQKKAASKGIND 411
 QY 367 EAVAGAAVOAAILMGDKSENVDLLIDVAPLSLGLETFAGVFWALIKNSTIPKQ 424
 Db 412 EAVAGAAVOAVGLSD -SDVADYLDVAVALLGLGLETFAGVFWALIKNSTIPKQ 469
 QY 427 IFTTYSNDQGVLYQVYEGERAKMDNLTGRELSGIPAPARGVQJEVTFDIDANG 485
 Db 470 IFTTYSNDQGVLYQVYEGERAKMDNLTGRELSGIPAPARGVQJEVTFDIDANG 529
 QY 487 WYATDSTGKANKTITNDKGRSKETIEBKVQAKKXKADQVOREVSANALBSYA 546
 Db 530 WYATDSTGKANKTITNDKGRSKETIEBKVQAKKXKADQVOREVSANALBSYA 589
 QY 547 FAKNKSAVED-BGLKNGKISEADKKRYLDKCOEYISMLDAPTLAKDEPFHKRELEJOYC 605
 Db 590 HSKKNQVND-LGRKLEEKREKTLIDAAVLEMLDNEPFAIEDPFKESLSKAVP 648
 QY 606 ITSGLYQAGRGPG 622
 Db 649 ITSGLYQAGRGPG 665

RESULT 8
 US-08-441-139-5
 / Sequence 5, Application US/08441139
 / Patent No. 5773245
 / GENERAL INFORMATION:
 / APPLICANT: Wiltup, Dr. Karl D.
 / APPLICANT: Robinson, Anne S.
 / TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
 / PROTEIN IN BACTERIA
 / TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
 / NUMBER OF SEQUENCES: 20
 / CORRESPONDENCE ADDRESS:
 / ADDRESS: SCULLY, SCOTT, MURPHY & PRESSER
 / STREET: 400 Garden City Plaza
 / CITY: Garden City
 / STATE: NY
 / COUNTRY: USA
 / ZIP: 11530
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / OPERATING SYSTEM: IBM PC compatible
 / SOFTWARE: PatentIn Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/441,139
 / FILING DATE: 15-MAY-1995

```

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,997
INVENTOR: SCOTT, MURPHY & PRESSER
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGLO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8646
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
FAX: 516-742-4366
TELEX: 230 901 USNR
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 679 amino acids
TYPE: amino acid
STANDARDNESS: single
MODIFIED: linear
MOLECULE TYPE: protein
US-08-441-139-5

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Query Match 59.7%; Score 1950.5; DB 1; Length 679;
Best Local Similarity 60.7%; Pred. No. 6,9e-151;
Matches 383; Conservative 102; Mismatches 133; Indels 13; Gaps 5;

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OY 1 AAAA-----AIGDGTTCSCVGVGRACKKEILANDQGNRTPTSPVATFTERLIG 52
DB 40 VARAEHDHYGVYIGDGLTTSVAMKMKTEILANDQGNRTPTSPVATFTERLIG 99
OY 53 DAANQVALNPORTVEPARLIGREFGDPVDSQDMHPFOVYINDGKPKVQSKGERK 112
DB 100 DAANQVALNPORTVEPARLIGREFGDPVDSQDMHPFOVYINDGKPKVQSKGERK 159
OY 113 AFPEPESVPTLTKWETAEKAYIGPTVMAVTVYRAYNDSONQATNDGATGANTLRI 172
DB 160 EEPPEVSMLIGKMKQIAEDYIGKKTAVYVYPAVNDQGNRTPTSPVATFTERLIG 219
OY 173 IEPTFAAIVAGLDITGKGERNVLIFPDGSPFVSSILITDGIPEVKAATGDTILGSD 232
DB 220 VHEPTAAIANGLDITGKGERNVLIFPDGSPFVSSILITDGIPEVKAATGDTILGSD 278
OY 223 PHEVTAHVEPEPKAKKEDISQNRANRLPTACERAKETSSQTSQASLETSLFEGID 292
DB 279 FYVLVRRHFOQLFKKHIDVATYNNOKMAKILREAKKATSSQTSQASLETSLFEGID 338
OY 293 FYTSITRAREELCSDFESTLEPEYKALBDKILDAQIHDVLYVGSSTRIPVYOKLLD 352
DB 339 FSETLIRAKREBELMLAFETKLPEVEYKLDGLOEIDIDVLYVGSSTRIPVYOKLLD 398
OY 353 PHEVTAHVEPEPKAKKEDISQNRANRLPTACERAKETSSQTSQASLETSLFEGID 412
DB 399 PFNCKAKSKGJNPDEAVAGAVALGCVLSGE--GVEVDIVLDVALITIGTGVMVP 456
OY 413 LKRNKSTIFPKOTQIFETYSQNGPGLIYVYGERKAKMKNLIGREFLSGIPPAKNGV 472
DB 457 LKRNKSTIFPKOTQIFETYSQNGPGLIYVYGERKAKMKNLIGREFLSGIPPAKNGV 516
OY 473 OLEVETDIDANGILNMTATDQSGAKNTITDNKORLAKSEETIPMVOYAKKAKPEQV 536
DB 517 OLEVETDIDANGILNMTATDQSGAKNTITDNKORLAKSEETIPMVOYAKKAKPEQV 576
OY 533 REHVSAKNALESYAFNNKSAVEDQKGIKISBAQKRYVLYKQCEVISMIDANF--LAKKE 591
DB 577 KAKSEKRNTEFNVEHYKNAVSQCE--LALIMDDQKTEVLYDNVNSLEMLDQNSDAAL 635
OY 592 FEHREKLEVOYCHPTISGLYOGAGRGPGCF 622
DB 636 FEHREKLEVOYCHPTISGLYOGAGRGPGCF 666

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RESULT 9
US-08-441-139-7
Sequence 7, Application US/08441139

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Patent No. 5773245
GENERAL INFORMATION:
APPLICANT: Millipore, Dr. Karl D.
TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSER: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: NEW YORK
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TRANSLATING SYSTEM: GENCOM
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,139
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,997
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGLO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8646
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
FAX: 516-742-4366
TELEX: 230 901 USNR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 663 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-441-139-7

```

```

Query Match 58.1%; Score 1897; DB 1; Length 663;
Best Local Similarity 59.5%; Pred. No. 1.6e-146;
Matches 365; Conservative 121; Mismatches 119; Indels 8; Gaps 7;

```

```

OY 7 IGLDGLTTSQCVGFQHGQVBIILANDQGNRTPTSPVATFTERLIGDAKQVALNPONT 66
DB 38 IGLDGLTTSQCVGFQHGQVBIILANDQGNRTPTSPVATFTERLIGDAKQVALNPONT 97
OY 67 VPDPAKYLIGKRGKDPVQVNDKMKHMPVOYINDGKPKVQSKGERKAFPEPESMVLK 126
DB 98 IEDKRLIGKRGKDPVQVNDKMKHMPVOYINDGKPKVQSKGERKAFPEPESMVLK 157
OY 127 MKETIAEVLGYPTNAVITVAFVNDSONQATNDGATGANTLRIINEPTAAIANGLD 186
DB 158 MKETIAEVLGYPTNAVITVAFVNDSONQATNDGATGANTLRIINEPTAAIANGLD 217
OY 187 PFGGGRANVLIFPDGSPFVSSILITDGIPEVKAATGDTILGSDPDRLVNHFVEERK 246
DB 218 KIVD--EKHIVLYDGLGTFVSLISIDNGVPEVLAISDGLGSDPDRLVNHFVEERK 276
OY 247 RHKKRDISQNRANRLPTACERAKETSSQTSQASLETSLFEGIDFYTSITRAREELC 306
DB 277 RHKKRDISQNRANRLPTACERAKETSSQTSQASLETSLFEGIDFYTSITRAREELC 336
OY 307 SOLPSTLEPEYKALBDKILDAQIHDVLYVGSSTRIPVYOKLLDPPNGDLNKSIND 366
DB 337 HOSLOEDPEPVOYKDSNLKKSSEIDIVLYVGSSTRIPVYOKLLDPPNGDLNKSIND 395
OY 367 EAVYAGAAVQAAILMKSGSEVODLLILNVAJLSLFTAGVMYALIRKSTIFPKOTQ 426
DB 396 EAVYAGAAVQAAILMKSGSEVODLLILNVAJLSLFTAGVMYALIRKSTIFPKOTQ 453

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OY 246 KRKHNDISQKRAVRLRTACERAKRTLSSSTQASLEISLFEQIDFYTSTIRARFEEI 305
DB 243 KRKHNDISQKRAVRLRTACERAKRTLSSSTQASLEISLFEQIDFYTSTIRARFEEI 301
OY 306 CSOLFSTLEPEKALDKAKLDKRAQJHDLVVGSTRI 343
DB 302 CADLFNSTLDPEKVLDAKDKLDSQVDEIVLVGSGTRI 339

RESUME 15
US-09-339-972-52
Sequence 52: Application US/09339972
GENERAL INFORMATION:
APPLICANT: Brody, Howard
APPLICANT: Vaver, Deborah S.
APPLICANT: Lamsa, Michael
APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods for Modifying the Production of
TITLE OF INVENTION: a Polypeptide
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESSES:
ADDRESSSEE: No. 63230020 No. 6323002disk of No. 6323002th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURSING AND INDEXING DATA:
APPLICATION NUMBER: 09/09/339,972
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/928,692
FILING DATE:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4944,200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SPO ID NO: 52:
SEQUENCE CHARACTERISTICS:
SEQUENCE LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6323002e
US-09-339-972-52

Query Match 41.5%, Score 1354, DB 4: Length 339:
Best Local Similarity 78.1%, PID 126-102:
Matches 264: Conservative 37; Mismatches 35; Indels 2; Gaps 2:

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OY 186 DRTGGERNVLIJEDGGTFPVSILITIDGIFEVKATAGDTHLGSEBPNRLVNHVEEP 245
DB 184 DKRG-BEVLILJEDGGTFPVSILFEQIDFVKATAGDTHLGSEBPNRLVNHVEEP 242
OY 246 KRKHNDISQKRAVRLRTACERAKRTLSSSTQASLEISLFEQIDFYTSTIRARFEEI 305
DB 243 KRKHNDISQKRAVRLRTACERAKRTLSSSTQASLEISLFEQIDFYTSTIRARFEEI 301
OY 306 CSOLFSTLEPEKALDKAKLDKRAQJHDLVVGSTRI 343
DB 302 CADLFNSTLDPEKVLDAKDKLDSQVDEIVLVGSGTRI 339

```

Search completed: December 4, 2002, 16:43:52
Job time : 18 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search using sw model

Run on: December 4, 2002, 16:40:57 : Search time 37 Seconds

(Without alignments) 3569,627 million cell updates/sec

Title: US-09-646-835-1

Sequence: 1 MAAKAAICIDLTGTYSCVGV.....PQAGCKGSGSGSPRIEWD 641

Scoring table:

Gapco 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : Listing first 45 summaries

1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.invertebrate:*
7: sp.invertebrate:*
8: sp.invertebrate:*
9: sp.phage:*
10: sp.plant:*
11: sp.fodent:*
12: sp.virus:*
13: sp.viridibacillaria:*
14: sp.viridibacillaria:*
15: sp.bacteriophage:*
16: sp.bacteriophage:*
17: sp.archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	3203.5	98.2	640	1	08WMS9
2	3203.5	98.2	640	1	08WMS9
3	3123.6	96.1	641	1	08WMS9
4	3114	95.4	642	1	08WMS9
5	2925	89.6	641	1	08WMS9
6	2889	88.5	641	1	08WMS9
7	2889	88.5	641	1	08WMS9
8	2826.5	86.6	646	13	073885
9	2826.5	86.6	646	13	073885
10	2800.5	85.4	639	13	080WMS
11	2792.5	85.6	650	13	073885
12	2792.5	85.6	650	13	073885
13	2789	85.5	658	13	091AC1
14	2789	85.5	658	13	091AC1
15	2787.5	85.4	644	13	080WMS

17	2778	85.1	649	13	P75984	P75984 brachydanio
18	2777	85.1	659	5	09XZJ2	09XZJ2 crassostrea
19	2763.5	84.7	638	13	080WMS	080WMS xiphophorus
20	2762.5	84.7	633	11	09YK07	09YK07 mus musculus
21	2758.5	84.5	658	5	027121	027121 urechis cau
22	2757	84.5	637	13	080WMS	080WMS xiphophorus
23	2757	84.5	637	13	080WMS	080WMS xiphophorus
24	2756	84.5	647	13	091993	091993 xenopus lae
25	2756	84.5	650	5	09GPK0	09GPK0 heterodera
26	2756	84.5	653	5	094805	094805 trichoplusia
27	2754.5	84.4	645	5	096541	096541 setaria diag
28	2753.5	84.4	645	5	09NCR9	09NCR9 tolu rufip
29	2752	84.3	639	4	083900	083900 tolu rufip
30	2752	84.3	639	4	083900	083900 tolu rufip
31	2747.5	84.2	645	5	09NCR9	09NCR9 tolu rufip
32	2745	84.1	653	5	017310	017310 cecartia c
33	2742.5	84.0	644	5	09NMX9	09NMX9 parasitomy
34	2730.5	83.7	640	5	093601	093601 caenorhabdi
35	2728	83.6	651	5	08SX04	08SX04 drosophila
36	2721	83.4	656	5	061226	061226 sycon rapia
37	2692	82.2	643	3	086118	086118 brachydanio
38	2692	82.2	643	3	086118	086118 brachydanio
39	2691	82.5	644	5	095477	095477 artelia san
40	2690.5	82.5	665	5	024789	024789 echinococcu
41	2685	81.7	646	5	001948	001948 trichinella
42	2634.5	80.7	663	5	024552	024552 geodia cydo
43	2619	80.3	645	13	091624	091624 xenopus lae
44	2567	79.1	566	6	095156	095156 macaca fasc
45	2567.5	78.7	586	4	096156	096156 homo sapien

ALIGNMENTS

RESULT 1	08WMS9	PRELIMINARY:	PRT:	640 AA.
AC	08WMS9			
DT	01-MAR-2002 (TREMBLrel. 20, Created)			
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Heat shock protein 70.			
DN	HSF70.			
OS	Canis familiaris (Dog).			
OC	Mammalia: Eutheria: Carnivora: Feliformia: Canidae: Canis			
NCBI_TaxID=9615;				
ON	[1]			
RP	SEQUENCE FROM N.A.			
RA	Abe K., Kano R., Hasegawa A.;			
RT	"Canine heat shock protein 70 (hsf70) mRNA, complete cds.";			
PL	Submitted (NOV-2001) to the EMBL/Genbank/DDBJ databases.			
DR	InterPro: IPR001023: Hsf70.			
DR	Prfam: PF00012: Hsf70: 1.			
DR	PRINTS: PR00301: HEATSHOCK70.			
DR	ProDom: PD000089: Hsf70: 1.			
DR	PROSITE: PS00297: Hsf70_1: UNKNOWN_1.			
DR	PROSITE: PS00329: Hsf70_2: UNKNOWN_1.			
DR	PROSITE: PS01036: Hsf70_3: UNKNOWN_1.			
SO	SEQUENCE 640 AA: 65935 MW: 40235918718P87F CRC64:			
Query Match	98.2%: Score 3203.5: DB 6: Length 640:			
Best Local Similarity	98.3%: Pred. No. 2.1e-174:			
Matches 630: Conservative 5: Mismatches 5: Indels 1: Gaps 1:				
Oy	1 MAAKAAICIDLTGTYSCVGVHGVVEIILANDGNETTPSYAFTPEKILGAAKNQYA 60			
Db	1 MAAKAAICIDLTGTYSCVGVHGVVEIILANDGNETTPSYAFTPEKILGAAKNQYA 60			
Oy	1 LNPONTVEFDKRLIGRPFDDVVSQDKMHPFVYVINDDDKPFVYVSKGDKAFPEIS 120			
Db	1 LNPONTVEFDKRLIGRPFDDVVSQDKMHPFVYVINDDDKPFVYVSKGDKAFPEIS 120			
Oy	61 LNPONTVEFDKRLIGRPFDDVVSQDKMHPFVYVINDDDKPFVYVSKGDKAFPEIS 120			
Db	61 LNPONTVEFDKRLIGRPFDDVVSQDKMHPFVYVINDDDKPFVYVSKGDKAFPEIS 120			

```

OY 121 SWLITFMKEIAEAYLGVPTNNATVTPAFVNDSDQATKNDAGVITAGLVANLEIINEPTAAA 180
Db 121 SWLITFMKEIAEAYLGVPTNNATVTPAFVNDSDQATKNDAGVITAGLVANLEIINEPTAAA 180
OY 181 IAGVLDRTGKGRNVNLPDLGGGTVDVSLITLIDGIFPEVAKADQTHLHGSDPDKRLVNH 240
Db 181 IAGVLDRTGKGRNVNLPDLGGGTVDVSLITLIDGIFPEVAKADQTHLHGSDPDKRLVNH 240
OY 241 PVEEPRFKHKKDIQSNKNAVRRLFAPEAKRKLSSSTQASLEIDSLFEGIDYSTSTA 300
Db 241 PVEEPRFKHKKDIQSNKNAVRRLFAPEAKRKLSSSTQASLEIDSLFEGIDYSTSTA 300
OY 241 PVEEPRFKHKKDIQSNKNAVRRLFAPEAKRKLSSSTQASLEIDSLFEGIDYSTSTA 300
Db 241 PVEEPRFKHKKDIQSNKNAVRRLFAPEAKRKLSSSTQASLEIDSLFEGIDYSTSTA 300
OY 301 REBELSDLPFRSTLEPEPEKALRDALDKAQIHDIYVVGSGSTRIPKQVLODFPFGNDLM 360
Db 301 REBELSDLPFRSTLEPEPEKALRDALDKAQIHDIYVVGSGSTRIPKQVLODFPFGNDLM 360
OY 361 KSINPEPVAVAGVANOALILMGKSENVODLLIDVAPLSLGLFAGVMTALIKRNSIT 420
Db 361 KSINPEPVAVAGVANOALILMGKSENVODLLIDVAPLSLGLFAGVMTALIKRNSIT 420
OY 421 PKOTQIFITYSNDPQVLIQVYESERAKTKNNLGFELSGIPAPRGVQITVTFDI 480
Db 421 PKOTQIFITYSNDPQVLIQVYESERAKTKNNLGFELSGIPAPRGVQITVTFDI 480
OY 481 DANQIILNTATDKSTGKARKTTTNDKGRSLKEEIRFVQVQAEKKAEDVQSRVSAKN 540
Db 481 DANQIILNTATDKSTGKARKTTTNDKGRSLKEEIRFVQVQAEKKAEDVQSRVSAKN 540
OY 541 ALESYAFNNKSAVEDGLKGISDARKKYLKCOBYISLANTLAEKDFEPRKRELE 600
Db 541 ALESYAFNNKSAVEDGLKGISDARKKYLKCOBYISLANTLAEKDFEPRKRELE 600
OY 601 QVCMPIISGLYOGAGCGPGCFGAGCPKGGSGSGPTTEBVD 641
Db 601 QVCMPIISGLYOGAGCGPGCFGAGCPKGGSGSGPTTEBVD 641
OY 641 QVCMPIISGLYOGAGCGPGCFGAGCPKGGSGSGPTTEBVD 641
Db 641 QVCMPIISGLYOGAGCGPGCFGAGCPKGGSGSGPTTEBVD 641

RESULT 2
O9QWU5 PRELIMINARY: PRT: 641 AA.
AC Q9QWU5 01-MAY-2000 (TREMUR-rel. 13. Created)
DT 01-MAY-2000 (TREMUR-rel. 13. Last annotation update)
DT 01-MAY-2002 (TREMUR-rel. 20. Last annotation update)
DE HSP70.
GN H2-BF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
OC SEQUENCE FROM N.A.
AC STRA1N-129;
RC Rowen L., Madan A., Qin S., Hall J., Dahl T., James R., Dickhoff R.,
RA Schaffer T., Ratcliffe A., Abbasi N., Loretz C., Lasky S., Hood L.;
*Sequence of the mouse MHC class III region.*
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF109506; GenBank: U01681; Fasta: The HART SHOCK PROTEIN 70 FAMILY.
EMBL: AF109506; NCBI_TaxID=10090;
DR HSP70.
DR HSP70; P08107; 1460.
DR MGD; MG1:105975; H2-BF.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70.1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000297; HSP70.1.1.
DR PROSITE; PS00329; HSP70.2; 1.
DR PROSITE; PS01036; HSP70.3; 1.
KW ATP-binding.
SO SEQUENCE 641 AA; 70079 MW; FA9C313602AE834 CRC64;
Query Match 96.1%; Score 3136; DB 11; Length 641;

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Best Local Similarity 95.3%; Pred. No. 1,Se-170;
Matches 611; Conservative 20; Mismatches 10; Indels 0; Gaps 0;
OY 1 MAAKAAIGDLGTFSCGVQHQKGVGLIANDGQRTTSSVYATPTRELLIDGAAKNOVA 60
Db 1 MAAKAAIGDLGTFSCGVQHQKGVGLIANDGQRTTSSVYATPTRELLIDGAAKNOVA 60
OY 61 LMPQNTVDKRLIGRKGDPVQSDMKAMPQVINDQDPKPVQVSYSGETKAPPEEIS 120
Db 61 LMPQNTVDKRLIGRKGDPVQSDMKAMPQVINDQDPKPVQVSYSGETKAPPEEIS 120
OY 120 LMPQNTVDKRLIGRKGDPVQSDMKAMPQVINDQDPKPVQVSYSGETKAPPEEIS 120
Db 120 LMPQNTVDKRLIGRKGDPVQSDMKAMPQVINDQDPKPVQVSYSGETKAPPEEIS 120
OY 121 SWLITFMKEIAEAYLGVPTNNATVTPAFVNDSDQATKNDAGVITAGLVANLEIINEPTAAA 180
Db 121 SWLITFMKEIAEAYLGVPTNNATVTPAFVNDSDQATKNDAGVITAGLVANLEIINEPTAAA 180
OY 181 IAGVLDRTGKGRNVNLPDLGGGTVDVSLITLIDGIFPEVAKADQTHLHGSDPDKRLVNH 240
Db 181 IAGVLDRTGKGRNVNLPDLGGGTVDVSLITLIDGIFPEVAKADQTHLHGSDPDKRLVNH 240
OY 241 PVEEPRFKHKKDIQSNKNAVRRLFAPEAKRKLSSSTQASLEIDSLFEGIDYSTSTA 300
Db 241 PVEEPRFKHKKDIQSNKNAVRRLFAPEAKRKLSSSTQASLEIDSLFEGIDYSTSTA 300
OY 301 REBELSDLPFRSTLEPEPEKALRDALDKAQIHDIYVVGSGSTRIPKQVLODFPFGNDLM 360
Db 301 REBELSDLPFRSTLEPEPEKALRDALDKAQIHDIYVVGSGSTRIPKQVLODFPFGNDLM 360
OY 361 KSINPEPVAVAGVANOALILMGKSENVODLLIDVAPLSLGLFAGVMTALIKRNSIT 420
Db 361 KSINPEPVAVAGVANOALILMGKSENVODLLIDVAPLSLGLFAGVMTALIKRNSIT 420
OY 421 PKOTQIFITYSNDPQVLIQVYESERAKTKNNLGFELSGIPAPRGVQITVTFDI 480
Db 421 PKOTQIFITYSNDPQVLIQVYESERAKTKNNLGFELSGIPAPRGVQITVTFDI 480
OY 481 DANQIILNTATDKSTGKARKTTTNDKGRSLKEEIRFVQVQAEKKAEDVQSRVSAKN 540
Db 481 DANQIILNTATDKSTGKARKTTTNDKGRSLKEEIRFVQVQAEKKAEDVQSRVSAKN 540
OY 541 ALESYAFNNKSAVEDGLKGISDARKKYLKCOBYISLANTLAEKDFEPRKRELE 600
Db 541 ALESYAFNNKSAVEDGLKGISDARKKYLKCOBYISLANTLAEKDFEPRKRELE 600
OY 601 QVCMPIISGLYOGAGCGPGCFGAGCPKGGSGSGPTTEBVD 641
Db 601 QVCMPIISGLYOGAGCGPGCFGAGCPKGGSGSGPTTEBVD 641
OY 641 QVCMPIISGLYOGAGCGPGCFGAGCPKGGSGSGPTTEBVD 641
Db 641 QVCMPIISGLYOGAGCGPGCFGAGCPKGGSGSGPTTEBVD 641

RESULT 3
O925V6 PRELIMINARY: PRT: 642 AA.
AC O925V6 01-DEC-2001 (TREMUR-rel. 19. Created)
DT 01-DEC-2001 (TREMUR-rel. 19. Last annotation update)
DT 01-DEC-2002 (TREMUR-rel. 20. Last annotation update)
DE HSP70.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
OC SEQUENCE FROM N.A.
AC STRA1N-129; Madan A., Qin S., Hall J., Dahl T., James R., Dickhoff R.,
RA Schaffer T., Ratcliffe A., Abbasi N., Loretz C., Lasky S., Hood L.;
*Sequence of the mouse MHC class III region.*
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF109506; GenBank: U01681; Fasta: The HART SHOCK PROTEIN 70 FAMILY.
EMBL: AF109506; NCBI_TaxID=10090;
DR HSP70.
DR InterPro; IPR000889; HSP70.1.
DR PRODOM; PD000089; HSP70.1.
DR PROSITE; PS00297; HSP70.1; UNKNOWN.1.

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TextID=9606;
RN
RP SEQUENCE FROM N.A.
RC
RT TISSUE=TESTIS;
RA MDLINE=98351992; PubMed=9685725;
RA Ito Y., Ando A., Ando H., Ando J., Saijoh Y., Inoko H., Fujimoto H.;
RA "Genomic structure of the spermatic-specific Hsp70 homolog gene
RA located in the class III region of the major histocompatibility
RA complex on human chromosome 12p13.3 (1998).
RL J. Biochem. 124:347-351(1998).
CC -1. SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; D85730; BAAB32521.1; -.
DR HSPSP; P08107; HSD.
DR Interpro; IP0001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PRINTS; PR00003; HSP70SHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
SQ
SEQUENCE 641 AA; 70437 MW; 303385E7D4301987 CRC64;
Query Match 89.68; Score 2925; DB 4; Length 641;
Best Local Similarity 89.48; PctIdent 125;
Matches 572; Conservative 34; Mismatches 16; Gaps 2;
QY 2 AAAAAAGIDAGTTTSCVGFQGHQKVEIIANDQGRTPTSVAFDTIERLIGDAARNOVAL 61
DB 4 AAGTALGIDAGTTTSCVGFQGHQKVEIIANDQGRTPTSVAFDTIERLIGDAARNOVAL 63
QY 62 NQMYTEPARLIGKRFQDPYVGNQMPYVNDGKRYVSKGKFAFYRETS 121
DB 62 NQMYTEPARLIGKRFQDPYVGNQMPYVNDGKRYVSKGKFAFYRETS 121
DB 64 NQMYTEPARLIGKRFQDPYVGNQMPYVNDGKRYVSKGKFAFYRETS 123
QY 122 NYLTKKEIEAVYAGPYNAVITVPAYFNDSQKATDAGVYAGNLVRIIEPTAAI 181
DB 122 NYLTKKEIEAVYAGPYNAVITVPAYFNDSQKATDAGVYAGNLVRIIEPTAAI 181
DB 124 NYLTKKEIEAVYAGPYNAVITVPAYFNDSQKATDAGVYAGNLVRIIEPTAAI 183
QY 184 AYGLDGTGGERNYLAFDLGGCTPPVSLITDGLFEYKATAGPMLGDEPNMLVNF 241
DB 184 AYGLDGTGGERNYLAFDLGGCTPPVSLITDGLFEYKATAGPMLGDEPNMLVNF 243
QY 242 VEEFKAKRKEDISONKRAVRRLTACRAKRTLSSTOASLEIDSLFEGIDEVTSITRAR 301
DB 242 VEEFKAKRKEDISONKRAVRRLTACRAKRTLSSTOASLEIDSLFEGIDEVTSITRAR 301
DB 244 VEEFKAKRKEDISONKRAVRRLTACRAKRTLSSTOASLEIDSLFEGIDEVTSITRAR 303
QY 302 FEELSCDLFSTLTPYEKALROKILDAQIHQIYVGGSTRIIPYVOKXILDFPNCRLK 361
DB 302 FEELSCDLFSTLTPYEKALROKILDAQIHQIYVGGSTRIIPYVOKXILDFPNCRLK 361
DB 304 FEELSCDLFSTLTPYEKALROKILDAQIHQIYVGGSTRIIPYVOKXILDFPNCRLK 363
QY 362 SINDEAVAGAQAVALIMKDKSENVQDILLDAVPSLGLETAGVYVALIKRNSITP 421
DB 362 SINDEAVAGAQAVALIMKDKSENVQDILLDAVPSLGLETAGVYVALIKRNSITP 421
DB 364 SINDEAVAGAQAVALIMKDKSENVQDILLDAVPSLGLETAGVYVALIKRNSITP 423
QY 422 TKQTOIFPTYSNDOPVLIQYEGBRAMKNNLLGRELISGTPPAAGVPOIETVFPD 481
DB 422 TKQTOIFPTYSNDOPVLIQYEGBRAMKNNLLGRELISGTPPAAGVPOIETVFPD 481
DB 424 TKQTOIFPTYSNDOPVLIQYEGBRAMKNNLLGRELISGTPPAAGVPOIETVFPD 483
QY 482 ANGLIWTATDSTGKANKTITINDKRLSKSEIEBWQVQAEKKADEVQBRYSAKNA 541
DB 482 ANGLIWTATDSTGKANKTITINDKRLSKSEIEBWQVQAEKKADEVQBRYSAKNA 541
DB 484 ANGLIWTATDSTGKANKTITINDKRLSKSEIEBWQVQAEKKADEVQBRYSAKNA 543
QY 544 LESAYANNAKSAVEDGLKGRISPAKAKYVLQKCOVSLMIDNLAKEDFEHKKRKEI 601
DB 544 LESAYANNAKSAVEDGLKGRISPAKAKYVLQKCOVSLMIDNLAKEDFEHKKRKEI 601
DB 544 LESAYANNAKSAVEDGLKGRISPAKAKYVLQKCOVSLMIDNLAKEDFEHKKRKEI 603
QY 602 VCAPITISGLYQAGGPGGNGAGPGGSG-----SGPTTEVD 641
DB 602 VCAPITISGLYQAGGPGGNGAGPGGSG-----SGPTTEVD 641
DB 604 MNPITITKLYQ-----GCTPACGTGTPAGRAATPTIEVD 641

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RESULT 6
QY 0960C9 PRELIMINARY; PRT: 641 AA.
DB 0960C9-2001 (TRENDArel. 19 Created)
DT 01-DEC-2001 (TRENDArel. 19 Last sequence update)
DT 01-MAR-2002 (TRENDArel. 20, Last annotation update)
DE Heat shock protein.
GN HSPAL1.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TextID=9606;
RN
RP SEQUENCE FROM N.A.
RC
RT TISSUE=TESTIS;
RA MDLINE=98351992; PubMed=9685725;
RA Ito Y., Ando A., Ando H., Ando J., Saijoh Y., Inoko H., Fujimoto H.;
RA "Genomic structure of the spermatic-specific Hsp70 homolog gene
RA located in the class III region of the major histocompatibility
RA complex on human chromosome 12p13.3 (1998).
RL J. Biochem. 124:347-351(1998).
CC -1. SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL; D85730; BAAB32521.1; -.
DR HSPSP; P08107; HSD.
DR Interpro; IP0001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PRINTS; PR00003; HSP70SHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding.
SQ
SEQUENCE 641 AA; 70405 MW; 303385E7D4300440 CRC64;
Query Match 89.68; Score 2925; DB 4; Length 641;
Best Local Similarity 89.48; PctIdent 125;
Matches 572; Conservative 34; Mismatches 16; Gaps 2;
QY 2 AAAAAAGIDAGTTTSCVGFQGHQKVEIIANDQGRTPTSVAFDTIERLIGDAARNOVAL 61
DB 4 AAGTALGIDAGTTTSCVGFQGHQKVEIIANDQGRTPTSVAFDTIERLIGDAARNOVAL 63
QY 62 NQMYTEPARLIGKRFQDPYVGNQMPYVNDGKRYVSKGKFAFYRETS 121
DB 62 NQMYTEPARLIGKRFQDPYVGNQMPYVNDGKRYVSKGKFAFYRETS 121
DB 64 NQMYTEPARLIGKRFQDPYVGNQMPYVNDGKRYVSKGKFAFYRETS 123
QY 122 NYLTKKEIEAVYAGPYNAVITVPAYFNDSQKATDAGVYAGNLVRIIEPTAAI 181
DB 122 NYLTKKEIEAVYAGPYNAVITVPAYFNDSQKATDAGVYAGNLVRIIEPTAAI 181
DB 124 NYLTKKEIEAVYAGPYNAVITVPAYFNDSQKATDAGVYAGNLVRIIEPTAAI 183
QY 184 AYGLDGTGGERNYLAFDLGGCTPPVSLITDGLFEYKATAGPMLGDEPNMLVNF 241
DB 184 AYGLDGTGGERNYLAFDLGGCTPPVSLITDGLFEYKATAGPMLGDEPNMLVNF 243
QY 242 VEEFKAKRKEDISONKRAVRRLTACRAKRTLSSTOASLEIDSLFEGIDEVTSITRAR 301
DB 242 VEEFKAKRKEDISONKRAVRRLTACRAKRTLSSTOASLEIDSLFEGIDEVTSITRAR 301
DB 244 VEEFKAKRKEDISONKRAVRRLTACRAKRTLSSTOASLEIDSLFEGIDEVTSITRAR 303
QY 302 FEELSCDLFSTLTPYEKALROKILDAQIHQIYVGGSTRIIPYVOKXILDFPNCRLK 361
DB 302 FEELSCDLFSTLTPYEKALROKILDAQIHQIYVGGSTRIIPYVOKXILDFPNCRLK 361
DB 304 FEELSCDLFSTLTPYEKALROKILDAQIHQIYVGGSTRIIPYVOKXILDFPNCRLK 363
QY 362 SINDEAVAGAQAVALIMKDKSENVQDILLDAVPSLGLETAGVYVALIKRNSITP 421
DB 362 SINDEAVAGAQAVALIMKDKSENVQDILLDAVPSLGLETAGVYVALIKRNSITP 421
DB 364 SINDEAVAGAQAVALIMKDKSENVQDILLDAVPSLGLETAGVYVALIKRNSITP 423
QY 422 TKQTOIFPTYSNDOPVLIQYEGBRAMKNNLLGRELISGTPPAAGVPOIETVFPD 481
DB 422 TKQTOIFPTYSNDOPVLIQYEGBRAMKNNLLGRELISGTPPAAGVPOIETVFPD 481
DB 424 TKQTOIFPTYSNDOPVLIQYEGBRAMKNNLLGRELISGTPPAAGVPOIETVFPD 483
QY 482 ANGLIWTATDSTGKANKTITINDKRLSKSEIEBWQVQAEKKADEVQBRYSAKNA 541
DB 482 ANGLIWTATDSTGKANKTITINDKRLSKSEIEBWQVQAEKKADEVQBRYSAKNA 541
DB 484 ANGLIWTATDSTGKANKTITINDKRLSKSEIEBWQVQAEKKADEVQBRYSAKNA 543

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OY 542 LESTVAENKSAVEDGDLKRGKISPAKRVLDKCOEYISMLDANFLAKOEPRHKKRELEDO 601
DB 544 LESTVAENKSAVEDGDLKRGKISPAKRVLDKCOEYISMLDANFLAKOEPRHKKRELEDO 603
OY 602 VCNPIITSLGXGAGPGRGCGAGCGAGCGAGG-----SGPTIEED 641
DB 604 MCNPITIKLYOG-----GCGAGCGAGGCGAGCGAGCGAGPTIEED 641

RESULT 7
OY 08686866 PRELIMINARY: PRT: 641 AA.
AC 0868686:
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Spermaticid-specific heat shock protein 70.
GN HSPAL1 OR HSC70P.
OS Mus musculus (Mouse).
OC Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RM [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C; TISSUE=TESTIS;
RC MEDLINE=9835192; PubMed=9685725;
RC LOC=11; Ando H., Ando H., Ando J., Saitoh Y., Inoko H., Fujimoto H.;
RC "Characterization of a cDNA encoding a member of the heat shock 70KD
RC protein family (HSP70) in axolotl."
RC located in the class III region of the major histocompatibility
RC complex of mouse and man."
RL J. Biochem. 124:347-353(1998).
CC 1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL: D85732; BAA32522.1; -.
DR BSSP: P08107; HSP70.
DR FEM: AF001012; HSP70.1.
DR MG: M61; 66231; HSP70.
DR PRODOM: P000089; HSP70.
DR PRINTS: PR00301; HEATSHOCK70.
DR PRODOM: P000089; HSP70.1.
DR PROSITE: PS00297; HSP70.2; 1.
DR PROSITE: PS00329; HSP70.3; 1.
DR PROSITE: PS01036; HSP70.3; 1.
DR AT: At-binding; Heat shock.
SQ SEQUENCE 641 AA; 70623 MW; D19B11742A03BCEP CRC64;

Query Match 88.5%; Score 2889; DB 11; Length 641;
Best Local Similarity 89.0%; Pred. Num. 1,7e+156;
Matches 569; Conservative 32; Mismatches 36; Indels 2; Gaps 2;

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OY 363 INDEAVAGAAVOAAILMDSKSEVENODLLLDVAAPLISGLEAGVYALIKRKNSTPT 422
DB 365 INDEAVAGAAVOAAILMDSKSEVENODLLLDVAAPLISGLEAGVYALIKRKNSTPT 424
OY 423 KQPIPTYSNDPOVLIQYEGGRAMRONNLGRRLDTIGIPPAQNGVPOIETPDDA 482
DB 425 KQPIPTYSNDPOVLIQYEGGRAMRONNLGRRLDTIGIPPAQNGVPOIETPDDA 484

OY 483 NGLINVAATDKSGKANKITINDOKRSLSEETREBVOAARVKADEQREBYSARKNA 542
DB 485 NGLINVAATDKSGKANKITINDOKRSLSEETREBVOAARVKADEQREBYSARKNA 544
OY 543 ESTVAENKSAVEDGDLKRGKISPAKRVLDKCOEYISMLDANFLAKOEPRHKKRELEDO 602
DB 545 ESTVAENKSAVEDGDLKRGKISPAKRVLDKCOEYISMLDANFLAKOEPRHKKRELEDO 604
OY 603 CNPIITSLGXGAGPGRGCGAGCGAGCGAGCGAGG-----SGPTIEED 641
DB 605 CNPIITIKLYOG-----GCGAGCGAGGCGAGCGAGCGAGPTIEED 641

RESULT 8
OY 08686866 PRELIMINARY: PRT: 651 AA.
AC 0868686:
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Spermaticid-specific heat shock protein 70.
GN HSPAL1 OR HSC70P.
OS Mus musculus (Mouse).
OC Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Salamandroides; Ambystomatidae;
OC Ambystoma.
OX NCBI_TaxID=8296;
RM [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C; TISSUE=TESTIS;
RC MEDLINE=9835192; PubMed=9685725;
RC LOC=11; Ando H., Ando H., Ando J., Saitoh Y., Inoko H., Fujimoto H.;
RC "Characterization of a cDNA encoding a member of the heat shock 70KD
RC protein family (HSP70) in axolotl."
RC located in the class III region of the major histocompatibility
RC complex of mouse and man."
RL J. Biochem. 124:347-353(1998).
CC 1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL: A092910; AKK1583.1; -.
DR BSSP: P08107; HSP70.
DR FEM: AF001012; HSP70.1.
DR MG: M61; 66231; HSP70.
DR PRODOM: P000089; HSP70.
DR PRINTS: PR00301; HEATSHOCK70.
DR PRODOM: P000089; HSP70.1.
DR PROSITE: PS00297; HSP70.2; UNKNOWN.1.
DR PROSITE: PS00329; HSP70.3; UNKNOWN.1.
DR PROSITE: PS01036; HSP70.3; UNKNOWN.1.
SQ SEQUENCE 651 AA; 71055 MW; 86C75FAD0CEFC9BD CRC64;

Query Match 86.7%; Score 2829; DB 13; Length 651;
Best Local Similarity 89.9%; Pred. Num. 6e+153;
Matches 553; Conservative 42; Mismatches 42; Indels 10; Gaps 4;

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DR EMBL: A0101312; CAA04673.1; -
 DR HSP70: P08109; ICR.
 DR Interpro: IPR001023; Hsp70.
 DR Pfam: PF00112; Hsp70.1.
 DR PRINTS: PR00101; Hsp70.1.
 DR PROSITE: PS00297; Hsp70.1.1.
 DR PROSITE: PS00297; Hsp70.2; 1.
 DR PROSITE: PS01036; Hsp70.3; 1.
 DR ATP-binding: 639 AA; 70292 MW; B296FA98407BD4AE CRC64;
 SQ SEQUENCE 639 AA: 70292 MW: B296FA98407BD4AE CRC64;
 Query Match 95.8%; Score 2820.5; Db 13; Length 639;
 Best Local Similarity 85.8%; Pred. No. 1.e-152;
 Matches 548; Conservative 47; Mismatches 41; Indels 3; Gaps 2;

QY 3 KAAAGIGDGGTTCVGVFGHKEVELIANDGKRTTSTVAFTDEIRLIDGAKNOVALN 62
 DR 1 KAAAGIGDGGTTCVGVFGHKEVELIANDGKRTTSTVAFTDEIRLIDGAKNOVALN 63
 QY 4 KGAAGIGDGGTTCVGVFGHKEVELIANDGKRTTSTVAFTDEIRLIDGAKNOVALN 63
 DR 4 KGAAGIGDGGTTCVGVFGHKEVELIANDGKRTTSTVAFTDEIRLIDGAKNOVALN 63
 QY 63 PNTVFARILIGRFEGPVSQSDMKLMPFKVINDGKRPVVOYEKGETKAFPEELISS 123
 DR 63 PNTVFARILIGRFEGPVSQSDMKLMPFKVINDGKRPVVOYEKGETKAFPEELISS 123
 QY 64 PNTVFARILIGRFEGPVSQSDMKLMPFKVINDGKRPVVOYEKGETKAFPEELISS 123
 DR 64 PNTVFARILIGRFEGPVSQSDMKLMPFKVINDGKRPVVOYEKGETKAFPEELISS 123
 QY 123 VLTNKEELIENAVLYGPTNANVTVPANFNDOSROATKDAVYAGLNTLRINEPTAAAI 182
 DR 123 VLTNKEELIENAVLYGPTNANVTVPANFNDOSROATKDAVYAGLNTLRINEPTAAAI 182
 QY 124 VLTNKEELIENAVLYGPTNANVTVPANFNDOSROATKDAVYAGLNTLRINEPTAAAI 183
 DR 124 VLTNKEELIENAVLYGPTNANVTVPANFNDOSROATKDAVYAGLNTLRINEPTAAAI 183
 QY 183 YGLDFTGKGEENVLYFDLGGTFPVSILITLEDGTFEVNSTADQTHLGGEDFDNRNWHF 242
 DR 183 YGLDFTGKGEENVLYFDLGGTFPVSILITLEDGTFEVNSTADQTHLGGEDFDNRNWHF 242
 QY 184 YGLDFTGKGEENVLYFDLGGTFPVSILITLEDGTFEVNSTADQTHLGGEDFDNRNWHF 243
 DR 184 YGLDFTGKGEENVLYFDLGGTFPVSILITLEDGTFEVNSTADQTHLGGEDFDNRNWHF 243
 QY 243 EEPKRRKKRDIISONKRAVERELTACERAKRTLSSTQASLEIDSLPEGIDFTSTTPARF 302
 DR 243 EEPKRRKKRDIISONKRAVERELTACERAKRTLSSTQASLEIDSLPEGIDFTSTTPARF 302
 QY 244 EEPKRRKKRDIISONKRAVERELTACERAKRTLSSTQASLEIDSLPEGIDFTSTTPARF 303
 DR 244 EEPKRRKKRDIISONKRAVERELTACERAKRTLSSTQASLEIDSLPEGIDFTSTTPARF 303
 QY 303 EELGSDLFRSTLEPYEKALRPAKADLIDVAPLSLGLTACVSTRLPRVOKTLODFNGENDLNK 362
 DR 303 EELGSDLFRSTLEPYEKALRPAKADLIDVAPLSLGLTACVSTRLPRVOKTLODFNGENDLNK 362
 QY 304 EELGSDLFRSTLEPYEKALRPAKADLIDVAPLSLGLTACVSTRLPRVOKTLODFNGENDLNK 363
 DR 304 EELGSDLFRSTLEPYEKALRPAKADLIDVAPLSLGLTACVSTRLPRVOKTLODFNGENDLNK 363
 QY 363 INPDEAVAGAVALIIMGKSENVODILLDVAFLSLGLTACVSTRLPRVOKTLODFNGENDLNK 422
 DR 363 INPDEAVAGAVALIIMGKSENVODILLDVAFLSLGLTACVSTRLPRVOKTLODFNGENDLNK 422
 QY 364 INPDEAVAGAVALIIMGKSENVODILLDVAFLSLGLTACVSTRLPRVOKTLODFNGENDLNK 423
 DR 364 INPDEAVAGAVALIIMGKSENVODILLDVAFLSLGLTACVSTRLPRVOKTLODFNGENDLNK 423
 QY 423 KOTQITFTYSNDQPGVLYVGEGRAMTKNNLIGFELSLGIFLAGVPAAPGVQVEVTFID 482
 DR 423 KOTQITFTYSNDQPGVLYVGEGRAMTKNNLIGFELSLGIFLAGVPAAPGVQVEVTFID 482
 QY 424 KOTQITFTYSNDQPGVLYVGEGRAMTKNNLIGFELSLGIFLAGVPAAPGVQVEVTFID 483
 DR 424 KOTQITFTYSNDQPGVLYVGEGRAMTKNNLIGFELSLGIFLAGVPAAPGVQVEVTFID 483
 QY 483 NGLINLTATDSTGKANKITINDKGRSLKEIRIVQASAKKAEDEVORENSAKAL 542
 DR 483 NGLINLTATDSTGKANKITINDKGRSLKEIRIVQASAKKAEDEVORENSAKAL 542
 QY 484 NGLINLTATDSTGKANKITINDKGRSLKEIRIVQASAKKAEDEVORENSAKAL 543
 DR 484 NGLINLTATDSTGKANKITINDKGRSLKEIRIVQASAKKAEDEVORENSAKAL 543
 QY 543 ESYAFAFMKSAVRBGLKISADKKKYLDKOCGVSYSLNATKLAEDPFRKRELEQ 601
 DR 543 ESYAFAFMKSAVRBGLKISADKKKYLDKOCGVSYSLNATKLAEDPFRKRELEQ 601
 QY 544 ESYAFAFMKSAVRBGLKISADKKKYLDKOCGVSYSLNATKLAEDPFRKRELEQ 603
 DR 544 ESYAFAFMKSAVRBGLKISADKKKYLDKOCGVSYSLNATKLAEDPFRKRELEQ 603
 QY 603 CWPTISGLYQAGGPGGFGAAGPGKGGSSGPTTEVD 641
 DR 603 CWPTISGLYQAGGPGGFGAAGPGKGGSSGPTTEVD 641
 QY 604 CWPTISGLYQAGGPGGFGAAGPGKGGSSGPTTEVD 642
 DR 604 CWPTISGLYQAGGPGGFGAAGPGKGGSSGPTTEVD 642

OC Pleuronectoidae; Paralichthyidae; Paralichthys.
 NCBI_Taxid=8255;
 RN [1]
 RA Tokoyama T., Hashimoto H., Rubota S., Kinoshita M., Toyohara H.,
 RA Nakamura T., Tanaka T., Sakai H., Kimura T.M.,
 RA Nakamura T., Tanaka T., Sakai H., Kimura T.M.,
 RA In Japanese Flounder Paralichthys olivaceus *;
 RL Fisheries Sci. 0:0-0(1999).
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
 DR EMBL: A010871; BAA1697.1; -
 DR HSP70: P08107; Hsp70.
 DR Interpro: IPR001023; Hsp70.
 DR PRINTS: PR00101; Hsp70.1.
 DR PROSITE: PS00297; Hsp70.1.1.
 DR PROSITE: PS00297; Hsp70.2; 1.
 DR PROSITE: PS01036; Hsp70.3; 1.
 DR ATP-binding: 640 AA; 70608 MW; 9C8B6573BFC0CT705 CRC64;
 SQ SEQUENCE 640 AA: 70608 MW: 9C8B6573BFC0CT705 CRC64;
 Query Match 95.8%; Score 2800.5; Db 13; Length 640;
 Best Local Similarity 84.2%; Pred. No. 1.9e-151;
 Matches 539; Conservative 59; Mismatches 39; Indels 3; Gaps 2;

QY 2 AKAAIGDGGTTCVGVFGHKEVELIANDGKRTTSTVAFTDEIRLIDGAKNOVALN 61
 DR 2 AKAAIGDGGTTCVGVFGHKEVELIANDGKRTTSTVAFTDEIRLIDGAKNOVALN 61
 QY 4 AKGIGDGGTTCVGVFGHKEVELIANDGKRTTSTVAFTDEIRLIDGAKNOVALN 63
 DR 4 AKGIGDGGTTCVGVFGHKEVELIANDGKRTTSTVAFTDEIRLIDGAKNOVALN 63
 QY 62 NPQNTVFADKRLIGRFEGPVSQSDMKLMPFKVINDGKRPVVOYEKGETKAFPEELISS 121
 DR 62 NPQNTVFADKRLIGRFEGPVSQSDMKLMPFKVINDGKRPVVOYEKGETKAFPEELISS 121
 QY 64 NPQNTVFADKRLIGRFEGPVSQSDMKLMPFKVINDGKRPVVOYEKGETKAFPEELISS 123
 DR 64 NPQNTVFADKRLIGRFEGPVSQSDMKLMPFKVINDGKRPVVOYEKGETKAFPEELISS 123
 QY 122 VLTNKEELIENAVLYGPTNANVTVPANFNDOSROATKDAVYAGLNTLRINEPTAAAI 181
 DR 122 VLTNKEELIENAVLYGPTNANVTVPANFNDOSROATKDAVYAGLNTLRINEPTAAAI 181
 QY 124 VLTNKEELIENAVLYGPTNANVTVPANFNDOSROATKDAVYAGLNTLRINEPTAAAI 183
 DR 124 VLTNKEELIENAVLYGPTNANVTVPANFNDOSROATKDAVYAGLNTLRINEPTAAAI 183
 QY 182 YGLDFTGKGEENVLYFDLGGTFPVSILITLEDGTFEVNSTADQTHLGGEDFDNRNWHF 241
 DR 182 YGLDFTGKGEENVLYFDLGGTFPVSILITLEDGTFEVNSTADQTHLGGEDFDNRNWHF 241
 QY 184 YGLDFTGKGEENVLYFDLGGTFPVSILITLEDGTFEVNSTADQTHLGGEDFDNRNWHF 243
 DR 184 YGLDFTGKGEENVLYFDLGGTFPVSILITLEDGTFEVNSTADQTHLGGEDFDNRNWHF 243
 QY 242 VEEFKRRKKRDIISONKRAVERELTACERAKRTLSSTQASLEIDSLPEGIDFTSTTPAR 301
 DR 242 VEEFKRRKKRDIISONKRAVERELTACERAKRTLSSTQASLEIDSLPEGIDFTSTTPAR 301
 QY 302 FEEELGSDLFRSTLEPYEKALRPAKADLIDVAPLSLGLTACVSTRLPRVOKTLODFNGENDLNK 361
 DR 302 FEEELGSDLFRSTLEPYEKALRPAKADLIDVAPLSLGLTACVSTRLPRVOKTLODFNGENDLNK 361
 QY 244 LEEFKRRKKRDIISONKRAVERELTACERAKRTLSSTQASLEIDSLPEGIDFTSTTPAR 303
 DR 244 LEEFKRRKKRDIISONKRAVERELTACERAKRTLSSTQASLEIDSLPEGIDFTSTTPAR 303
 QY 304 FEEELGSDLFRSTLEPYEKALRPAKADLIDVAPLSLGLTACVSTRLPRVOKTLODFNGENDLNK 363
 DR 304 FEEELGSDLFRSTLEPYEKALRPAKADLIDVAPLSLGLTACVSTRLPRVOKTLODFNGENDLNK 363
 QY 362 INPDEAVAGAVALIIMGKSENVODILLDVAFLSLGLTACVSTRLPRVOKTLODFNGENDLNK 421
 DR 362 INPDEAVAGAVALIIMGKSENVODILLDVAFLSLGLTACVSTRLPRVOKTLODFNGENDLNK 421
 QY 364 INPDEAVAGAVALIIMGKSENVODILLDVAFLSLGLTACVSTRLPRVOKTLODFNGENDLNK 423
 DR 364 INPDEAVAGAVALIIMGKSENVODILLDVAFLSLGLTACVSTRLPRVOKTLODFNGENDLNK 423
 QY 422 TKOTQITFTYSNDQPGVLYVGEGRAMTKNNLIGFELSLGIFLAGVPAAPGVQVEVTFID 481
 DR 422 TKOTQITFTYSNDQPGVLYVGEGRAMTKNNLIGFELSLGIFLAGVPAAPGVQVEVTFID 481
 QY 424 TKOTQITFTYSNDQPGVLYVGEGRAMTKNNLIGFELSLGIFLAGVPAAPGVQVEVTFID 483
 DR 424 TKOTQITFTYSNDQPGVLYVGEGRAMTKNNLIGFELSLGIFLAGVPAAPGVQVEVTFID 483
 QY 482 ANGLINLTATDSTGKANKITINDKGRSLKEIRIVQASAKKAEDEVORENSAKANA 541
 DR 482 ANGLINLTATDSTGKANKITINDKGRSLKEIRIVQASAKKAEDEVORENSAKANA 541
 QY 484 ANGLINLTATDSTGKANKITINDKGRSLKEIRIVQASAKKAEDEVORENSAKANA 543
 DR 484 ANGLINLTATDSTGKANKITINDKGRSLKEIRIVQASAKKAEDEVORENSAKANA 543
 QY 542 LESYAFAMKSAVRBGLKISADKKKYLDKOCGVSYSLNATKLAEDPFRKRELEQ 601
 DR 542 LESYAFAMKSAVRBGLKISADKKKYLDKOCGVSYSLNATKLAEDPFRKRELEQ 601
 QY 544 LESYAFAMKSAVRBGLKISADKKKYLDKOCGVSYSLNATKLAEDPFRKRELEQ 603
 DR 544 LESYAFAMKSAVRBGLKISADKKKYLDKOCGVSYSLNATKLAEDPFRKRELEQ 603
 QY 602 CWPTISGLYQAGGPGGFGAAGPGKGGSSGPTTEVD 641
 DR 602 CWPTISGLYQAGGPGGFGAAGPGKGGSSGPTTEVD 641
 QY 604 WCPITVTKLYQGA -APPG -OSSGAGGAGNAGPTTEVD 640
 DR 604 WCPITVTKLYQGA -APPG -OSSGAGGAGNAGPTTEVD 640

RESULT 12

08JUN99

[illegible][illegible]

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Oy 63 PONTVEDAKRLIOMKFGDDPWOSSMKHPPQVIMODNKPKYOVSTKGEKATPEEISSM 122
Db 65 PUNTVIDAKRLIQRHFDDBPVYQSDMKHNSKIVYSDGKPVAVBHKGBKTFMPEEISSM 124
Oy 123 VLTMRKEIAEAYIGPVTNAVITVPAYPNDSORQATKDAVITAGLNVLTINPTAAATA 182
Db 125 VLTMRKEIAEAYIGOKVTNAVITVPAYPNDSORQATKDAVITAGLNVLTINPTAAAP 184
Oy 183 YGLDRGKGERNVLLFDLGCGSTEDVSLI71DGLFEVKATAGTHLGEDDKRLVNHFY 242
Db 185 YGLDKGKSSERNVLLFDLGCGSTEDVSLITEDGIFVMAINAGTHLGEDEDNBVNHFY 244
Oy 243 EEFRRKHKKDISQNRRAVBRLPACERAKRTLSSSTOASLETDLSPEGIDPYSTTRAP 302
Db 245 EEFRRKHKKDISQNRRLRLPACERAKRTLSSSSOASLEIDSLEYGIDPYSTTRAP 304
Oy 303 EELCSDFRSTLEPEKALRDANKLRQAQIHDLVUGGSTRIPEVOKLLODFPNGBDLNKS 362
Db 305 EELCSDFRSTLDVPEKALRQKHKRQAQIHDLVUGGSTRIPEKLNLODFPNGBDLNKS 364
Oy 363 IMPDEAVNAGVAOAILMGDKSENVODLILADVAPLSIGLETFAGVMTALIKRNSTIPT 422
Db 365 IMPDEAVNAGVAOAILMGDTSONVODLILADVAPLSIGLETFAGVMTALIKRNTIPT 424
Oy 423 KOTQITTTSDNQPCVLIQVTEBRRAMTKNNLLGFEELSGIPEAPPGVPOIEVTFDIDA 482
Db 425 KOTQITTTSDNQPCVLIQVTEBRRAMTKNNLLGFEELSGIPEAPPGVPOIEVTFDIDA 484
Oy 483 NGILNTATATDSTGKANKITTTNDKGRLSKEEIRRWQOEAEKRAEDVOEREVSANKNL 542
Db 485 NGILNTASANDSTGOKRITTTNDKGRLSKEEIRRWQOEPADMYKAEDDLQREKISANKNL 544
Oy 543 ESYAFPMKSAVEDPGIKGKISGAEKKYALDKGCVTSLDAMTLAREDEBKKELEBOY 602
Db 545 ESYAFPMKSSVEDDMLKGRISEDDKRYIEKCNQAVSWLENNOQLADRETEHQLEKEY 604
Oy 603 CNPITISGLYQAGCGPGGFGAGCPKGGSG--SGPTIE 638
Db 605 CNPVTISRLYO--GMPAGGCGAQO--RQASGPAALGPPILK 640

```

Search Completed: December 4, 2002, 16:43:29
 Job time : 39 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 16:40:37 : Search time 21 seconds
(without alignments)
2934.389 Million cell updates/sec

Title: US-09-646-835-1

Perfect score: 1263.1
Sequence: 1 MAKAAMGIDLTGTYSCGVY.....FGAQPKGSGSGRTTEYD 641

Scoring table:

Gapop 10.0 , Gaepext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3263	100	641	A45871	dnak-type molecule
2	3242.5	99.4	641	A29161	dnak-type molecule
3	3216	98.6	641	SS3357	dnak-type molecule
4	3182	97.5	641	S35718	dnak-type molecule
5	3169	97.1	641	I54542	dnak-type molecule
6	3148.5	96.5	638	S31766	dnak-type molecule
7	3123.5	95.8	642	DR0095	dnak-type molecule
8	3085.5	93.8	642	DR0095	dnak-type molecule
9	2884	88.7	641	T49761	dnak-type molecule
10	2882	88.3	641	S41415	dnak-type molecule
11	2862.5	87.7	646	S07197	dnak-type molecule
12	2862.5	87.7	646	JC4853	dnak-type molecule
13	2859.5	87.6	646	A27077	dnak-type molecule
14	2856.5	87.5	646	S31716	dnak-type molecule
15	2853.5	87.5	650	S45362	dnak-type molecule
16	2853.5	87.5	650	S45362	dnak-type molecule
17	2843.5	87.1	646	A35922	dnak-type molecule
18	2835.5	86.9	647	1 BHM170	dnak-type molecule
19	2816	86.3	651	S21175	dnak-type molecule
20	2800.5	85.8	640	T43724	dnak-type molecule
21	2798	85.7	643	S25585	dnak-type molecule
22	2772.5	85.0	639	A55718	dnak-type molecule
23	2762	84.8	634	A32142	dnak-type molecule
24	2757.5	84.5	633	S10859	dnak-type molecule
25	2757.5	84.5	633	S10859	dnak-type molecule
26	2751.5	84.3	633	S08211	dnak-type molecule
27	2747	84.2	643	S09036	dnak-type molecule
28	2735	83.8	644	A45635	dnak-type molecule
29	2730.5	83.7	640	T21394	hypothetical prote

ALIGNMENTS

Result 1
A: A45871
M: Alternate names: heat shock protein HSP70-1 - human
C: Species: Homo sapiens (man)
C: Date: 03-Mar-1994 #sequence, revision 03-Mar-1994 #text, change 20-Aug-1999
C: Accession: A45871
R: Miller, C.M.; Campbell, R.D.
J Biol Chem 269:15119-15126 (1994)
A: Reference number: A45871; MID:91055806; PMID:1700760
A: Accession: A45871
A: Status: Preliminary
A: Molecule type: DNA
A: Residues: 1-641 <X11>
A: Cross-References: GB:959828; GB:M34207; NID:q188487; PIDN:MAA63226.1; PID:q188488;
A: Description: Involved in protein folding and assembling/disassembling of protein co
C: Keywords: ATP; molecular chaperone

Query Match 100.0%; Score 3263; DB 2; Length 641;
Best Local Similarity 100.0%; Pred. No. 2e-173;
Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAKAAMGIDLTGTYSCGVYQHKVYVIAANDGKRTTSPVAPTFRRILIDMAKKVYA	60
DB	1	MAKAAMGIDLTGTYSCGVYQHKVYVIAANDGKRTTSPVAPTFRRILIDMAKKVYA	60
QY	61	LNFQNTVEDAKRLGIRGKQPPVSDSKIMPFQVITNDGKPPVSDVYSGETAAFPRETS	120
DB	61	LNFQNTVEDAKRLGIRGKQPPVSDSKIMPFQVITNDGKPPVSDVYSGETAAFPRETS	120
QY	121	SMVLTNKKKEIAEAVLYGVYNNVAVYFVNDSDQATKNDGAVIAGLVLRILINPTMAA	180
DB	121	SMVLTNKKKEIAEAVLYGVYNNVAVYFVNDSDQATKNDGAVIAGLVLRILINPTMAA	180
QY	241	FVEEERKHKDIQONKRAVRLRFADEAKRFLSSQASLEIDSEIDIFFTSTSTA	300
DB	241	FVEEERKHKDIQONKRAVRLRFADEAKRFLSSQASLEIDSEIDIFFTSTSTA	300
QY	301	FEELCDLSPSTLEPEVKALDKAAIDHLYVNGSTRIPKYOALQDFPENGRLN	360
DB	301	FEELCDLSPSTLEPEVKALDKAAIDHLYVNGSTRIPKYOALQDFPENGRLN	360
QY	361	KSLNPEAVAGAVOAAILMGSKSEWODLLILVAPISGLGTFAGVFWALIKRSTI	420
DB	361	KSLNPEAVAGAVOAAILMGSKSEWODLLILVAPISGLGTFAGVFWALIKRSTI	420
QY	420	361 KSLNPEAVAGAVOAAILMGSKSEWODLLILVAPISGLGTFAGVFWALIKRSTI	420
DB	420	361 KSLNPEAVAGAVOAAILMGSKSEWODLLILVAPISGLGTFAGVFWALIKRSTI	420

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Oy 421 PRKOTLFTTYSNPGVLIQVIEGERRAKRNNMLGRFELSGDIPPAKGVQVLTETFD 480
Db 421 PRKOTLFTTYSNPGVLIQVIEGERRAKRNNMLGRFELSGDIPPAKGVQVLTETFD 480
Oy 481 DANCILMTATDTSKGRANKITITNDKGRISKEEIEHWQAEARKKAEDEVQREYSAN 540
Db 481 DANCILMTATDTSKGRANKITITNDKGRISKEEIEHWQAEARKKAEDEVQREYSAN 540
Oy 541 ALESTAFNNKSAVEDELKGRKISBAKKRYLDKQCEVISMWDLANTLAEDFEHKKKELE 600
Db 541 ALESTAFNNKSAVEDELKGRKISBAKKRYLDKQCEVISMWDLANTLAEDFEHKKKELE 600
Oy 601 QVNCPIISGLYOGAGCGPGCGAOGPGCGSGGSPPTIERVD 641
Db 601 QVNCPIISGLYOGAGCGPGCGAOGPGCGSGGSPPTIERVD 641

RESULT 2
A23160
dnak-type molecular chaperone HSPAL1 - human
N:Alternate names: heat shock protein, 70K
C:Species: Homo sapiens (man)
C>Date: 16-Aug-1988 #sequence_revision 02-Jul-1996 #lexl_change 20-Aug-1999
C:Accession: A29160; 137561; 137562
R:Name, C: MORTIMOO, R.I. A. 82, 6455-6459, 1985
A:Title: Conserved features of eukaryotic hsp70 genes revealed by comparison with the nu
A:Reference number: A29160; MUID:86018721; PMID:3931075
A:Accession: A29160
A:Molecule type: DNA
A:Residues: 1-640 <HUN>
A:Cross-references: GB:M1117; GB:M15432; NID:9184416; PID:AAA52697.1; PID:9386785
A:Note: The authors mistranslated residues 463, 491, and 492
Molecule: Res 16, 8933-8948, 1986
A:Title: In vitro transcription of a human hsp 70 heat shock gene by extracts prepared f
A:Reference number: 137561; MUID:87066768; PMID:3786441
A:Accession: 137561
A>Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-640 <HUN>
A:Cross-references: EMBL:X04676; NID:932480; PID:CAA2381.1; PID:932481
A:Accession: 137562
A>Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 616-640 <RE2>
A:Cross-references: EMBL:X04677; NID:932402; PID:CAA2382.1; PID:932483
A:Accession: 137562
A:Gene: HSPAL1; HSP70-HOM
A:Cross-references: GDB:120058; OMIM:140559
A:Map position: 6p21.3-6p21.3
A:Mutations: #status absent
C:Function:
A:Description: Involved in protein folding and assembling/disassembling of protein comp
A:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone
Query Match 99.4%; Score 3242.5; DB 2: Length 640;
Best Local Similarity 99.5%; Pred. No. 2.7e-111;
Matches 638; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

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Oy 181 IAVGLDTRKGEENVALFDLGGSTEDVSLITLDGILEPKKATAGDTLGGSDPDKMLVN 240
Db 181 IAVGLDTRKGEENVALFDLGGSTEDVSLITLDGILEPKKATAGDTLGGSDPDKMLVN 240
Oy 241 FVEEKKRKKRSDSONKRAVRLRFACRRKRTSSSTQASLEIDSLFEGIDEPYSITRA 300
Db 241 FVEEKKRKKRSDSONKRAVRLRFACRRKRTSSSTQASLEIDSLFEGIDEPYSITRA 300
Oy 301 REELSGDLPSTLPEYKARLMDKLMKQIIMDLVYGQSTRIPVOKLLDDFPNKSOLA 360
Db 301 REELSGDLPSTLPEYKARLMDKLMKQIIMDLVYGQSTRIPVOKLLDDFPNKSOLA 360
Oy 361 KSIINDEAAVGAAYOVALITMKGDSFNQDILLDAAPLSLGLFAGYVVALILKRNSTI 420
Db 361 KSIINDEAAVGAAYOVALITMKGDSFNQDILLDAAPLSLGLFAGYVVALILKRNSTI 420
Oy 421 PRKOTLFTTYSNPGVLIQVIEGERRAKRNNMLGRFELSGDIPPAKGVQVLTETFD 480
Db 421 PRKOTLFTTYSNPGVLIQVIEGERRAKRNNMLGRFELSGDIPPAKGVQVLTETFD 480
Oy 481 DANCILMTATDTSKGRANKITITNDKGRISKEEIEHWQAEARKKAEDEVQREYSAN 540
Db 481 DANCILMTATDTSKGRANKITITNDKGRISKEEIEHWQAEARKKAEDEVQREYSAN 540
Oy 541 ALESTAFNNKSAVEDELKGRKISBAKKRYLDKQCEVISMWDLANTLAEDFEHKKKELE 600
Db 540 ALESTAFNNKSAVEDELKGRKISBAKKRYLDKQCEVISMWDLANTLAEDFEHKKKELE 599
Oy 601 QVNCPIISGLYOGAGCGPGCGAOGPGCGSGGSPPTIERVD 641
Db 600 QVNCPIISGLYOGAGCGPGCGAOGPGCGSGGSPPTIERVD 640

RESULT 3
A53357
dnak-type molecular chaperone hsp70 - bovine
N:Alternate names: 70K heat shock protein
C:Species: Bos primigenius taurus (cattle)
C>Date: 05-Dec-1999 #sequence_revision 05-Dec-1998 #lexl_change 21-Jul-2000
C:Accession: S53357; Overlapped IT, V.
A:Reference number: 53357; MUID:95126904; PMID:1826329
A:Accession: S53357
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-641 <G77>
A:Cross-references: EMBL:U09861; NID:94397937; PID:AAA3914.1; PID:94397938
A:Map position: 30A.1-30A.2, 1995
A:Title: Chemical modifications of a recombinant bovine stress-inducible 70 kDa heat-
A:Reference number: 53357; MUID:95126904; PMID:1826329
A:Accession: S53357
C:Function:
A:Description: Involved in protein folding and assembling/disassembling of protein co
A:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone
Query Match 98.8%; Score 3216; DB 2: Length 641;
Best Local Similarity 98.8%; Pred. No. 7.9e-110;
Matches 633; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

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Db 598 QVNCPIISGLYOGAGPGEPSGFGAOGPKGSGSPFTIEVD 638

RESULT 7

drak-type molecular chaperone hsp70 - mouse

N:Alternate names: heat shock protein 70

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 20-Aug-1999

C:Accession: J00095

R:Rat, C.: Calderwood, S.

Gene 87, 209-224, 1990

A:Status: preliminary

A:Accession: J00095

A:Molecule type: DNA

A:Residues: 1-642 <HND>

A:Cross-references: GB:M35021; NID:9194023; PIDN:AAA37864.1; PID:9387211

A:Experimental source: strain A7

C:Function: involved in protein folding and assembling/dissembly of protein complex

C:Superfamily: heat shock protein 70

C:Keywords: ATP; molecular chaperone

Query Match 95.8%; Score 3125.5; Db 2; Length 642;

Best Local Similarity 95.2%; Pred. No. 7.9e-165;

Matches 611; Conservative 20; Mismatches 10; Indels 1; Gaps 1;

1 MAAATAGTGGTTCVGVQHGKVEITANDGQNTFTPSVAFDTEELIGDAKNQVAL 60

1 MAANTAGTGGTTCVGVQHGKVEITANDGQNTFTPSVAFDTEELIGDAKNQVAL 60

61 LNPQTVFPAKRLIGKRFCDPVVOSDMKMPQVINDGKEKQVSYKGTAKAFPEIS 120

61 LNPQTVFPAKRLIGKRFCDPVVOSDMKMPQVINDGKEKQVSYKGTAKAFPEIS 120

61 LNPQTVFPAKRLIGKRFCDPVVOSDMKMPQVINDGKEKQVSYKGTAKAFPEIS 120

121 SMTLTKKEIAEAYLGPTNANVTVPAYFNDGROATKAGVAGLNLINETPAAI 180

121 SMTLTKKEIAEAYLGPTNANVTVPAYFNDGROATKAGVAGLNLINETPAAI 180

121 SMTLTKKEIAEAYLGPTNANVTVPAYFNDGROATKAGVAGLNLINETPAAI 180

181 IAVGLDRTGKGRNVLIFDLAGGTFPVSLITDDGIFEVKATAGDTHLGGEDPNRLVNH 240

181 IAVGLDRTGKGRNVLIFDLAGGTFPVSLITDDGIFEVKATAGDTHLGGEDPNRLVNH 240

181 IAVGLDRTGKGRNVLIFDLAGGTFPVSLITDDGIFEVKATAGDTHLGGEDPNRLVNH 240

241 FVEEKKRKKKIDSONKRAVRELTACERAKRTLSSTQASLEIDSEIGDIFTSITRA 300

241 FVEEKKRKKKIDSONKRAVRELTACERAKRTLSSTQASLEIDSEIGDIFTSITRA 300

301 REBELCSDLFSTLPEVEKALRDAKLDAKQAHDLVAGSGFRIIPKQKALQDPFNDRDLN 360

301 REBELCSDLFSTLPEVEKALRDAKLDAKQAHDLVAGSGFRIIPKQKALQDPFNDRDLN 360

301 REBELCSDLFSTLPEVEKALRDAKLDAKQAHDLVAGSGFRIIPKQKALQDPFNDRDLN 360

361 KSTNPDEAVAGAAVQALILMGKRSBNVODLLIDVALSLGIFGAGVMAALIKRNSITP 420

361 KSTNPDEAVAGAAVQALILMGKRSBNVODLLIDVALSLGIFGAGVMAALIKRNSITP 420

361 KSTNPDEAVAGAAVQALILMGKRSBNVODLLIDVALSLGIFGAGVMAALIKRNSITP 420

421 PTKQTFPTTYSNPGVLIQVYEGEERAMTKDNLLRRELSTGIPARNGVQALIEVTDI 480

421 PTKQTFPTTYSNPGVLIQVYEGEERAMTKDNLLRRELSTGIPARNGVQALIEVTDI 480

421 PTKQTFPTTYSNPGVLIQVYEGEERAMTKDNLLRRELSTGIPARNGVQALIEVTDI 480

481 DANGILVATADSKTGKANKITITNKGRLSKETIEEMVOAEKRYAKEDVEERKRELE 540

481 DANGILVATADSKTGKANKITITNKGRLSKETIEEMVOAEKRYAKEDVEERKRELE 540

481 DANGILVATADSKTGKANKITITNKGRLSKETIEEMVOAEKRYAKEDVEERKRELE 540

541 ALESAFNKSAVDEGLAKLISDAKRVVLKCEVTSMDANTLAKEDVEERKRELE 600

541 ALESAFNKSAVDEGLAKLISDAKRVVLKCEVTSMDANTLAKEDVEERKRELE 600

541 ALESAFNKSAVDEGLAKLISDAKRVVLKCEVTSMDANTLAKEDVEERKRELE 600

601 QVNCPIISGLYOGAGPGEPSGFGAOGPKGSGSPFTIEVD 641

601 QVNCPIISGLYOGAGPGEPSGFGAOGPKGSGSPFTIEVD 641

601 QVNCPIISGLYOGAGPGEPSGFGAOGPKGSGSPFTIEVD 641

Db 601 QVNCPIISGLYOGAGPGEPSGFGAOGPKGSGSPFTIEVD 642

RESULT 8

B45871

drak-type molecular chaperone HSP70-Hom - human

N:Alternate names: heat shock protein HSP70-Hom

C:Species: Homo sapiens (man)

C:Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 20-Aug-1999

C:Accession: B45871

R:Miller, C.M.; Campbell, R.D.

Immunogenetics 32, 242-251, 1990

A:Title: Structure and expression of the three MHC-linked HSP70 genes.

A:Reference number: B45871; MUID:9105806; PMID:1700760

A:Accession: B45871

A:Status: preliminary

A:Residues: 1-641 <HND>

A:Cross-references: GB:M59829; GB:M34268; NID:9188491; PIDN:AAA63228.1; PID:9188492

A:Description: involved in protein folding and assembling/dissembly of protein complex

C:Superfamily: heat shock protein 70

C:Keywords: ATP; molecular chaperone

Query Match 90.5%; Score 2921; Db 2; Length 641;

Best Local Similarity 88.3%; Pred. No. 1.5e-155;

Matches 571; Conservative 34; Mismatches 26; Indels 16; Gaps 2;

2 AKAAATGIDGTTTCVGVQHGKVEITANDGQNTFTPSVAFDTEELIGDAKNQVAL 61

2 AKAAATGIDGTTTCVGVQHGKVEITANDGQNTFTPSVAFDTEELIGDAKNQVAL 61

4 AKQATAGTGGTTCVGVQHGKVEITANDGQNTFTPSVAFDTEELIGDAKNQVAL 63

62 NPQTVFPAKRLIGKRFCDPVVOSDMKMPQVINDGKEKQVSYKGTAKAFPEIS 121

64 NPQTVFPAKRLIGKRFCDPVVOSDMKMPQVINDGKEKQVSYKGTAKAFPEIS 123

122 SMTLTKKEIAEAYLGPTNANVTVPAYFNDGROATKAGVAGLNLINETPAAI 181

122 SMTLTKKEIAEAYLGPTNANVTVPAYFNDGROATKAGVAGLNLINETPAAI 181

122 SMTLTKKEIAEAYLGPTNANVTVPAYFNDGROATKAGVAGLNLINETPAAI 181

182 AVGLDRTGKGRNVLIFDLAGGTFPVSLITDDGIFEVKATAGDTHLGGEDPNRLVNH 241

182 AVGLDRTGKGRNVLIFDLAGGTFPVSLITDDGIFEVKATAGDTHLGGEDPNRLVNH 241

182 AVGLDRTGKGRNVLIFDLAGGTFPVSLITDDGIFEVKATAGDTHLGGEDPNRLVNH 241

184 AVGLDRTGKGRNVLIFDLAGGTFPVSLITDDGIFEVKATAGDTHLGGEDPNRLVNH 243

242 VEEFKRKKKIDSONKRAVRELTACERAKRTLSSTQASLEIDSEIGDIFTSITRA 301

242 VEEFKRKKKIDSONKRAVRELTACERAKRTLSSTQASLEIDSEIGDIFTSITRA 301

242 VEEFKRKKKIDSONKRAVRELTACERAKRTLSSTQASLEIDSEIGDIFTSITRA 301

302 FVEEKKRKKKIDSONKRAVRELTACERAKRTLSSTQASLEIDSEIGDIFTSITRA 361

302 FVEEKKRKKKIDSONKRAVRELTACERAKRTLSSTQASLEIDSEIGDIFTSITRA 361

302 FVEEKKRKKKIDSONKRAVRELTACERAKRTLSSTQASLEIDSEIGDIFTSITRA 361

361 KSTNPDEAVAGAAVQALILMGKRSBNVODLLIDVALSLGIFGAGVMAALIKRNSITP 421

361 KSTNPDEAVAGAAVQALILMGKRSBNVODLLIDVALSLGIFGAGVMAALIKRNSITP 421

361 KSTNPDEAVAGAAVQALILMGKRSBNVODLLIDVALSLGIFGAGVMAALIKRNSITP 421

422 TTKQTFPTTYSNPGVLIQVYEGEERAMTKDNLLRRELSTGIPARNGVQALIEVTDI 481

422 TTKQTFPTTYSNPGVLIQVYEGEERAMTKDNLLRRELSTGIPARNGVQALIEVTDI 481

422 TTKQTFPTTYSNPGVLIQVYEGEERAMTKDNLLRRELSTGIPARNGVQALIEVTDI 481

424 PTKQTFPTTYSNPGVLIQVYEGEERAMTKDNLLRRELSTGIPARNGVQALIEVTDI 483

482 ANGLVATADSKTGKANKITITNKGRLSKETIEEMVOAEKRYAKEDVEERKRELE 541

482 ANGLVATADSKTGKANKITITNKGRLSKETIEEMVOAEKRYAKEDVEERKRELE 541

482 ANGLVATADSKTGKANKITITNKGRLSKETIEEMVOAEKRYAKEDVEERKRELE 541

542 LESAFAFNKSAVDEGLAKLISDAKRVVLKCEVTSMDANTLAKEDVEERKRELE 601

542 LESAFAFNKSAVDEGLAKLISDAKRVVLKCEVTSMDANTLAKEDVEERKRELE 601

542 LESAFAFNKSAVDEGLAKLISDAKRVVLKCEVTSMDANTLAKEDVEERKRELE 601

602 VCNCPISGLYOGAGPGEPSGFGAOGPKGSGSPFTIEVD 641

602 VCNCPISGLYOGAGPGEPSGFGAOGPKGSGSPFTIEVD 641

604 MGNPTIISGLYOGAGPGEPSGFGAOGPKGSGSPFTIEVD 641

Db 604 MGNPTIISGLYOGAGPGEPSGFGAOGPKGSGSPFTIEVD 641

RESULT 9

149761

drak-type molecular chaperone Hsc70c - mouse

N:Alternate names: heat shock protein 70
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Aug-1996 #sequence=rev150n 02-Aug-1996 #text-change 20-Aug-1999
 C:Accession: S41415
 R:Accession: 015761, M.G.; van Vugt, H.; Milner, C.M.; Toucher, C.; Campbell, R.D.
 Immunogenetics 40:159-162, 1994
 A:Title: Coding sequences and levels of expression of Hsc70t are identical in mice with
 A:Reference number: 149761, MUID:94299288, PMID:8026864
 A:Accession: 149761
 A:Status: preliminary; translated from GB/EMBL/DDDBJ
 A:Molecule type: DNA
 A:Gene: Hsc70
 A:Cross-references: GB:U7086; NID:9457299; PIDD:AA53936.1; PTD:9457300
 C:Function:
 A:Description: involved in protein folding and assembling/dissassembling of protein comp
 C:Superfamily: heat shock protein 70
 C:Keywords: ATP; molecular chaperone

Query Match 88.7% Score 2894; DB 2; Length 641;
 Best Local Similarity 89.2%; Pidd. No. 4,5a-152;
 Matches 570; Conservative 32; Mismatches 35; Indels 2; Gaps 2;

Oy 3 KAAATGIDGTTSCVGVFOHAKVETIANDQGNTPSYAFTDTEBLIGDAKKNQYALN 62
 Db 5 KQNAITGIDGTTSCVGVFOHAKVETIANDQGNTPSYAFTDTEBLIGDAKKNQYALN 64
 Oy 63 PONTVDANKRLIGRKFGDPVYQSDMKHPPTVINDQDTPKPYOSKGTAKAPPEETSSM 122
 Db 65 PONTVDANKRLIGRKFGDPVYQSDMKHPPTVINDQDTPKPYOSKGTAKAPPEETSSM 124
 Oy 123 VLTMKETLAEAYIGPYTAAVTVPAFENDSROAKRQACVAGLNLITNEPTAALN 182
 Db 125 VLTMKETLAEAYIGPYTAAVTVPAFENDSROAKRQACVAGLNLITNEPTAALN 184
 Oy 183 YGLDRGKGERNYLFDLGGGTGDSITLTDGJFEVAKATAGDHLGEGDPRNLVHRY 242
 Db 185 YGLDRGKGERNYLFDLGGGTGDSITLTDGJFEVAKATAGDHLGEGDPRNLVHRY 244
 Oy 243 EEFRRKHKKDISONKRAVRLRPLACERAKKTLSSTQASLEIDSLFPGIDETYSITRAEP 302
 Db 245 EEFRRKHKKDISONKRAVRLRPLACERAKKTLSSTQASLEIDSLFPGIDETYSITRAEP 304
 Oy 303 EELCSDFPESTLEPEVAKLRPAKLDQAHIDVYVSGSTRIPRYOKLDDPFNGDLNKS 362
 Db 305 EELCSDFPESTLEPEVAKLRPAKLDQAHIDVYVSGSTRIPRYOKLDDPFNGDLNKS 364
 Oy 423 KOTQITFTTSDNPGVLIQVYEEERAMRNKLGLGFELSGIPPAKPGVPIETVFDIDA 482
 Db 425 KOTQITFTTSDNPGVLIQVYEEERAMRNKLGLGFELSGIPPAKPGVPIETVFDIDA 484
 Oy 483 KQILNLTATDSYGANKTTTNDKRLSSEETIRAWDEAKYAEDEVQSERVANKAL 542
 Db 485 KQILNLTATDSYGANKTTTNDKRLSSEETIRAWDEAKYAEDEVQSERVANKAL 544
 Oy 543 ESYAFPNKSAVEDGLKGTISEADKKYLDKQCOVSYMLDANTLAEKDFEHRKELEOV 602
 Db 545 ESYAFPNKSAVEDGLKGTISEADKKYLDKQCOVSYMLDANTLAEKDFEHRKELEOV 604
 Oy 603 CNPTITSLQYAGAGGFGFAGQKGGSGSGPTTEVD 641
 Db 605 CNPTITSLQYAGAGGFGFAGQKGGSGSGPTTEVD 641

RESULT 10
 S41415
 dark-type molecular chaperone Hsp70.3 - rat
 N:Alternate names: heat shock protein 70

C:Species: Rattus norvegicus (Norway rat)
 C>Date: 06-Jan-1995 #sequence=rev150n 06-Jan-1995 #text-change 21-Jul-2000
 C:Accession: S41415; 168987
 R:Accession: S41415, MUID:94299288, PMID:8026864
 A:Title: Coding sequences and levels of expression of Hsc70t are identical in mice with
 A:Reference number: 149761, MUID:94299288, PMID:8026864
 A:Accession: S41415
 A:Molecule type: DNA
 A:Gene: Hsc70
 A:Cross-references: EMBL:X77209; NID:91814002; PIDD:CAAN54424.1; PTD:9450934
 R:Walter, L.; Rauh, F.; Gunther, E.
 Immunogenetics 40:159-162, 1994
 A:Reference number: 154542; MUID:95012453; PMID:7927536
 A:Accession: 169987
 A:Status: preliminary; translated from GB/EMBL/DDDBJ
 A:Molecule type: DNA
 A:Gene: Hsc70
 A:Cross-references: EMBL:X77209; NID:91814002; PIDD:CAAN54424.1; PTD:9450934
 C:Function:
 A:Description: involved in protein folding and assembling/dissassembling of protein co
 C:Superfamily: heat shock protein 70
 C:Keywords: ATP; molecular chaperone

Query Match 88.3% Score 2682; DB 2; Length 641;
 Best Local Similarity 89.2%; Pidd. No. 4,5a-152;
 Matches 569; Conservative 32; Mismatches 33; Indels 8; Gaps 3;

Oy 3 KAAATGIDGTTSCVGVFOHAKVETIANDQGNTPSYAFTDTEBLIGDAKKNQYALN 62
 Db 5 KQNAITGIDGTTSCVGVFOHAKVETIANDQGNTPSYAFTDTEBLIGDAKKNQYALN 64
 Oy 63 PONTVDANKRLIGRKFGDPVYQSDMKHPPTVINDQDTPKPYOSKGTAKAPPEETSSM 122
 Db 65 PONTVDANKRLIGRKFGDPVYQSDMKHPPTVINDQDTPKPYOSKGTAKAPPEETSSM 124
 Oy 123 VLTMKETLAEAYIGPYTAAVTVPAFENDSROAKRQACVAGLNLITNEPTAALN 182
 Db 125 VLTMKETLAEAYIGPYTAAVTVPAFENDSROAKRQACVAGLNLITNEPTAALN 184
 Oy 183 YGLDRGKGERNYLFDLGGGTGDSITLTDGJFEVAKATAGDHLGEGDPRNLVHRY 242
 Db 185 YGLDRGKGERNYLFDLGGGTGDSITLTDGJFEVAKATAGDHLGEGDPRNLVHRY 244
 Oy 243 EEFRRKHKKDISONKRAVRLRPLACERAKKTLSSTQASLEIDSLFPGIDETYSITRAEP 302
 Db 245 EEFRRKHKKDISONKRAVRLRPLACERAKKTLSSTQASLEIDSLFPGIDETYSITRAEP 304
 Oy 303 EELCSDFPESTLEPEVAKLRPAKLDQAHIDVYVSGSTRIPRYOKLDDPFNGDLNKS 362
 Db 305 EELCSDFPESTLEPEVAKLRPAKLDQAHIDVYVSGSTRIPRYOKLDDPFNGDLNKS 364
 Oy 423 KOTQITFTTSDNPGVLIQVYEEERAMRNKLGLGFELSGIPPAKPGVPIETVFDIDA 482
 Db 425 KOTQITFTTSDNPGVLIQVYEEERAMRNKLGLGFELSGIPPAKPGVPIETVFDIDA 484
 Oy 483 KQILNLTATDSYGANKTTTNDKRLSSEETIRAWDEAKYAEDEVQSERVANKAL 542
 Db 485 KQILNLTATDSYGANKTTTNDKRLSSEETIRAWDEAKYAEDEVQSERVANKAL 544
 Oy 543 ESYAFPNKSAVEDGLKGTISEADKKYLDKQCOVSYMLDANTLAEKDFEHRKELEOV 602
 Db 545 ESYAFPNKSAVEDGLKGTISEADKKYLDKQCOVSYMLDANTLAEKDFEHRKELEOV 604
 Oy 603 CNPTITSLQYAGAGGFGFAGQKGGSGSGPTTEVD 641
 Db 605 CNPTITSLQYAGAGGFGFAGQKGGSGSGPTTEVD 641

Qy	421	PKPTQLEFYSNDQPGVLQYVGGRRAMKNNLIGRELISGIPPARARVQLEWTEVI	480
Dy	421	PKPTQLEFYSNDQPGVLQYVGGRRAMKNNLIGRELISGIPPARARVQLEWTEVI	480
Qy	481	DANGLIANTVATDKSTGAKMLITTDNGRLAKSEELIEWQDAKTKADPEVRYSAN	540
Dy	481	DANGLIANTVATDKSTGAKMLITTDNGRLAKSEELIEWQDAKTKADPEVRYSAN	540
Qy	541	ALSEVYFNNKSAVEDDEGLGKTSKADKRYLQCGVITSMIDANLTAJKPEERKRELE	600
Dy	541	ALSEVYFNNKSAVEDDEGLGKTSKADKRYLQCGVITSMIDANLTAJKPEERKRELE	600
Qy	601	QWCPWITISGLYQAGG-PG--PGAG--GAQGRGSSSSPTTEVD	641
Dy	601	KVCPHTIKLYQAGGPGAMPGRPGAGAPISGQASGPTTIEDV	646

RESULT 13

A27077

dnak-type molecular chaperone - human

C:Alternate names: heat shock cognate protein 70

C:Source: human (man)

C:Date: 19-Nov-1988

C:Accession: A27077

R:Domonczak, B.: Mitaule, M.E.

Nucleic Acids Res. 15, 5181-5197, 1987

A:Title: Structure and expression of a human gene coding for a 71 kd heat shock cognate protein

A:Accession: A27077

A:Reference number: A27077; MUID:87259994; PMID:3037489

A:Accession type: DNA

A:Realtime type: cDNA

A:Cross-references: GB:M19141

C:Genetics:

A:introns: 69/1; 137/3; 188/3; 374/1; 441/3; 508/1; 585/3

C:Function:

A:Description: involved in protein folding and assembling/dissassembling of protein comp

C:Superfamily: heat shock protein 70

C:Keywords: ATP; molecular chaperone

Query Match

Best Local Similarity 85.6%; Score 2859.5; DB 2; Length 646;

Matches 553; Conservative 48; Mismatches 40; Indels 5; Gaps 3;

Db	421	PKKOTFTTYS	DNQD	POVYLIOVVEE	EEBA	MTKNNLKG	AFGLTCLG	IPAPG	PGD	LE	TF	DI	480
Qy	481	DANGL	ANT	MTK	STG	KANK	TTTTND	KGR	LS	EE	IE	EE	540
Db	481	DNQD	ANT	MTK	STG	KANK	TTTTND	KGR	LS	EE	IE	EE	540
Qy	541	ATSEY	AP	PM	K	S	AV	PE	GL	K	I	E	600
Db	541	STSEY	AP	PM	K	S	AV	PE	GL	K	I	E	600
Qy	601	QYCN	PT	IS	GL	YQ	AG	PG	PG	PG	PG	641	
Db	601	KYCN	PT	IS	GL	YQ	AG	PG	PG	PG	PG	641	
RESULT 14													
		531716											
		dnak_type	molecular	chaperone	hsp72-ps1	-	rat						
		C:species	Natus	norvegicus	(Norway Rat)								
		C:accession	U61329		GenBank	13-Jan-1995	1	text_change	20-Aug-1999				
		R:writer	L. Helne	L. Gauthier	E.								
		Immunogenetics	39	351-354	1994								
		A:file	Sequence	expression	and mapping of a rat Mbc class Ib gene.								
		A:reference number	160329	MUID:94222444	PMID:7545923								
		A:accession	160329										
		A:submitter	PELHIM29										
		A:submitter	PELHIM29										
		A:residues	1646	<RES>									
		A:cross-references	EMBL:X70065	NID:g56384	PIDN:CAA91670.1	PII:g56385							
		C:gene	hsp72-ps1										
		C:function											
		A:description	Involved in protein folding and assembling/dissassembling of protein										
		A:supernatant	Heat shock protein 72										
		C:keywords	ATP	molecular chaperone									
Qy	1	MAR	KA	IS	IS	IS	IS	IS	IS	IS	IS	60	
Db	1	MSK	RA	VS	IS	IS	IS	IS	IS	IS	IS	60	
Qy	61	LMP	ON	VS	ED	AK	IS	IS	IS	IS	IS	120	
Db	61	NMP	NT	VS	ED	AK	IS	IS	IS	IS	IS	120	
Qy	121	SMV	TK	ET	AK	IS	IS	IS	IS	IS	IS	180	
Db	121	SMV	TK	ET	AK	IS	IS	IS	IS	IS	IS	180	
Qy	181	I	AV	LD	RT	GR	IS	IS	IS	IS	IS	240	
Db	181	I	AV	LD	RT	GR	IS	IS	IS	IS	IS	240	
Qy	241	P	IE	ER	K	AK	IS	IS	IS	IS	IS	300	
Db	241	P	IE	ER	K	AK	IS	IS	IS	IS	IS	300	
Qy	301	P	IE	ER	K	AK	IS	IS	IS	IS	IS	360	
Db	301	P	IE	ER	K	AK	IS	IS	IS	IS	IS	360	
Qy	361	K	S	I	N	D	P	E	A	V	A	420	
Db	361	K	S	I	N	D	P	E	A	V	A	420	
Qy	421	P	K	R	O	T	F	T	T	S	D	480	
Db	421	P	K	R	O	T	F	T	T	S	D	480	

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 16:47:44 : Search time 14 Seconds
(without alignments)
1899.023 Million cell updates/sec

Title: US-09-646-835-1

Sequence: 1 MNRMAAIDIDGTTTCYGV.....FGAGPFGKSGSGGTIEVD 641

Scoring table:

OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size: 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64.1	100.0	641	1 HS71_HUMAN	P08107 homo sapien
2	370	57.7	641	1 HS71_BOVIN	027975 bos taurus
3	370	57.7	641	1 HS72_BOVIN	027965 bos taurus
4	375	22.6	634	1 HS71_MOUSE	034930 sus scrofa
5	114	17.8	641	1 HS71_PIG	007435 porc sus
6	114	17.8	641	1 HS71_PIG	007435 porc sus
7	101	15.8	641	1 HS71_MOUSE	P17879 mus musculu
8	80	12.5	420	1 HS71_MOUSE	061696 mus musculu
9	57	8.9	639	1 HS71_ORYLA	091879 oryzias lat
10	55	8.6	633	1 HS72_MOUSE	P17156 mus musculu
11	25	8.6	633	1 HS72_RAT	P14659 rattus norv
12	8	8.6	634	1 HS72_CHICK	P08106 gallus gall
13	8	8.6	634	1 HS72_CHICK	P55063 rattus norv
14	55	8.6	641	1 HS71_PIG	P34931 homo sapien
15	55	8.6	641	1 HS71_HUMAN	P16627 mus musculu
16	55	8.6	641	1 HS71_MOUSE	091233 oncorhynch
17	55	8.4	644	1 HS70_ORYLA	P11347 cyrtolus
18	53	8.3	646	1 HS7C_CRGR	P11347 cyrtolus
19	53	8.3	646	1 HS7C_HUMAN	P08107 mus musculu
20	53	8.3	649	1 HS70_MOUSE	090473 brachyante
21	53	8.3	649	1 HS7C_BRAHE	P19120 bos taurus
22	53	8.3	650	1 HS7C_BOVIN	P11147 diosophila
23	53	8.3	651	1 HS7D_DROME	094691 oryzias lat
24	53	8.3	651	1 HS7D_DROME	P22632 paracentrot
25	53	8.3	652	1 HS7C_ORYLA	P34933 bos taurus
26	50	7.8	378	1 HS72_PAB1	P14827 anopheles a
27	47	7.3	631	1 HS72_BOVIN	P14827 anopheles a
28	44	7.3	651	1 HS70_HUMAN	P08108 mus musculu
29	44	7.3	651	1 HS70_HUMAN	P08108 mus musculu
30	43	6.7	645	1 HS70_PIGMA	P02826 diosophila
31	42	6.6	379	1 HS7X_PIG	P02826 diosophila
32	42	6.6	643	1 HS7E_PIG	P27541 brugia mala
33	42	6.6	653	1 HS72_ARATH	P36415 dicystostell

ALIGNMENTS

RESULT 1	ID	HS71_HUMAN	STANDARD:	PERT:	641 AA.
AC	P08107	6191790	Q90040	Q90040	
DE	01-FEB-1994	(Rel. 28)	Last sequence update		
DE	15-JUN-2002	(Rel. 41)	Last annotation update		
DE	Heat shock 70 kDa protein 1 (HSP70.1) (HSP70-1/HSP70-2).				
GN	(HSPAL1 OR HSPAL1) AND HSPAL1B.				
OS	homo sapiens (human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
PN	111...Taxid=9606;				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-91055806; PubMed-1700760;				
RA	Milner C.M., Campbell R.D.;				
RT	"Structure and expression of the three MHC-linked HSP70 genes."				
RL	Immunogenetics 32:242-251(1990).				
RN	111...Taxid=9606;				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-86016721; PubMed-3931075;				
RA	Hunt C., Morimoto R.I.;				
RT	"Conserved features of eukaryotic hsp70 genes revealed by comparison with the nucleotide sequence of human hsp70."				
RL	Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).				
RN	131...Taxid=9606;				
RP	SEQUENCE FROM N.A. (HSPAL1 AND HSPAL1B).				
RA	Abbas N., Dichtoff R., Loretz C., Madan A., Jors M., Young J.;				
RT	"Sequence of the human major histocompatibility complex class III region."				
RL	Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.				
RN	141...Taxid=9606;				
RP	SEQUENCE FROM N.A. (HSPAL1 AND HSPAL1B).				
RX	MEDLINE-89184548; PubMed-2538823;				
RA	Sargent C.A., Dunham I., Rowlands J., Campbell R.D.;				
RT	"Heat shock protein HSP70.1: a family complex contains genes for the major heat shock protein HSP70."				
RL	Proc. Natl. Acad. Sci. U.S.A. 86:1968-1972(1989).				
RN	161...Taxid=9606;				
RP	SEQUENCE OF 1-22 AND 618-641 FROM N.A.				
RX	MEDLINE-87066768; PubMed-3786141;				
RA	Drabent B., Gentile A., Benke B.-J.;				
RT	"In vitro transcription of a human hsp 70 heat shock gene by extracts from human cells."				
RL	Nucleic Acids Res. 14:8933-8949(1986).				
RN	171...Taxid=9606;				
RP	X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-382.				
RX	MEDLINE-99234376; PubMed-10216320;				

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CC EMBL: AF268675; AAF91485.1; -
 DR HSPSP: P08109; ICR.
 DR InterPro: IPR001023; Hsp70.
 DR Pfam: PF00012; Hsp70.1.
 DR PRINTS: P600301; Hsp70CK70.
 DR PROSITE: PS00297; Hsp70.1.1.
 DR PROSITE: PS00329; Hsp70.2.1.
 DR PROSITE: PS01036; Hsp70.3.1.
 DR ATP-binding; Heat shock; Multigene family.
 KW SEQUENCE 639 AA: 70350 MW: 61047E0DD0EB0534 CRC64;
 SO

Query Match 8.9% Score 57; DB 1; Length 639;
 Best Local Similarity 100.0%; Pred. No. 2,4e-49;
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 9 I GIDGTTTCVGVPGHGVKEIIANDGQNTPTSYVAFDTERLIGDAKNOVA 65
 9 I GIDGTTTCVGVPGHGVKEIIANDGQNTPTSYVAFDTERLIGDAKNOVA 65

RESULT 10
 ID HSP72.MOUSE STANDARD; PRT: 633 AA.
 AC P17156;
 DT 01-NOV-1990 (Rel. 15, Created)
 DT 01-NOV-1990 (Rel. 15, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DR HSP72.MOUSE: Hsp72 protein 2 (heat shock protein 70.2).
 OS HSP72 OR HSP70 (Hsp70.2).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN 11)
 RP SEQUENCE FROM N.A.
 RA Baker, J. S. (1992) Pubmed=340524;
 RA Baker, J. S. (1992) C. R. ;
 RT Identification and sequence analysis of a new member of the mouse
 RT HSP70 gene family and characterization of its unique cellular and
 RT developmental pattern of expression in the male germ line.*;
 RL Mol. Cell. Biol. 8:2925-2932(1988).
 CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
 CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
 CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
 CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN THE CELLULAR RESPONSE
 CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATION OF
 CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
 CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
 CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
 CC -1- DEVELOPMENTAL STAGE: SPECIFICALLY EXPRESSED IN PROPHAGE STAGE
 CC
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch)

CC EMBL: M20567; AAA37859.1; -
 DR PTR: S10859; S10859.
 DR HSPSP: P19120; IATR.
 DR InterPro: IPR001023; Hsp70.
 DR

DR Pfam: PF00012; Hsp70.1.
 DR PRINTS: P600301; Hsp70CK70.
 DR PROSITE: PS00297; Hsp70.1.1.
 DR PROSITE: PS00329; Hsp70.2.1.
 DR PROSITE: PS01036; Hsp70.3.1.
 DR ATP-binding; Chaperone; Heat shock; Multigene family.
 KW SEQUENCE 633 AA: 69740 MW: E7P904F2A8138D CRC64;
 SO

Query Match 8.6% Score 55; DB 1; Length 633;
 Best Local Similarity 100.0%; Pred. No. 2,4e-47;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 6 A IIGDITTCVGVPGHGVKEIIANDGQNTPTSYVAFDTERLIGDAKNOVA 60
 6 A IIGDITTCVGVPGHGVKEIIANDGQNTPTSYVAFDTERLIGDAKNOVA 61

RESULT 11
 ID HSP72.RAT STANDARD; PRT: 633 AA.
 AC P14659;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DR HSP72.RAT: Hsp72 protein 2 (heat shock protein 70.2) (Testis-
 DE specific heat shock protein-related) (HSP7).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxId=10116;
 RN 11)
 RP SEQUENCE FROM N.A.
 RA Strain-Sprague-Dawley; Tissue-Liver;
 RA Baker, J. S. (1992) Pubmed=340524;
 RA Baker, J. S. (1992) C. R. ;
 RT Isolation and nucleotide sequence analysis of the rat
 RT testis-specific major heat-shock protein (HSP70)-related gene.*;
 RL Bloch, M. (1988) Acta 1048:93-99(1988).
 CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
 CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
 CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
 CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN THE CELLULAR RESPONSE
 CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATION OF
 CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
 CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
 CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
 CC
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CC EMBL: X15705; CAA37355.1; -
 DR PTR: S09211; S09211.
 DR HSPSP: P19120; 3HSC.
 DR InterPro: IPR001023; Hsp70.
 DR Pfam: PF00012; Hsp70.1.
 DR PRINTS: P600301; Hsp70CK70.
 DR PROSITE: PS00297; Hsp70.1.1.
 DR PROSITE: PS00329; Hsp70.2.1.
 DR PROSITE: PS01036; Hsp70.3.1.
 DR ATP-binding; Chaperone; Heat shock; Multigene family;
 KW Spermatogenesis.
 SO SEQUENCE 633 AA: 69528 MW: 68786ACCEB8P7DA CRC64;
 Query Match 8.6% Score 55; DB 1; Length 633;

RN	[1]
RP	SEQUENCE FROM N.A.
RA	MEDLINE-9513016; PubMed-7823106;
RB	Bornycastle L.L.C.; Yu C.-E., Hunt C.R., Trask B.J., Clancy K.P.,
RC	Lundquist G.D., Drenth J.G., Scheraga H.A., et al. "Cloning,
RD	"Cloning," sequencing, and mapping of the human chromosome 14 heat
RE	shock protein gene (<i>HSPA2</i>). "
RF	Genomics 23:85-93(1994).
RG	[12]
RH	SEQUENCE FROM N.A.
RI	Gorski R.T.J., Kravsky A.M.: The EMBL/GenBank/DDJJ databases.
RJ	Submitted (Apr-1996) to the EMBL/Genbank/DDDJ databases.
RK	SEQUENCE OF 1-126 FROM N.A.
RL	MEDLINE-95152505; PubMed-7849706;
RM	Roux A.-F., Nguyen V.T.T., Squire J.A., Cox D.W.:
RN	A heat shock gene at 14q22: mapping and expression."
RO	Hum. Mol. Genet. 3:1819-1822(1994).
RR	-1 PUNCTION IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
RS	PERSISTENT PROTEINS AGAINST AGGREGATION AND MODULATE THE FOLDING
RT	KINETICS OF DENATURATION. THESE RESULTS INDICATE THAT THESE PROCESSES
RU	OCCUR THROUGHOUT THE CELLULAR RESPONSE TO HEAT SHOCK AND ARE INVOLVED
RV	THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF
RW	OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
RX	HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
RY	AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
RZ	-1 SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
SAC	FUNTS-PSS-PROT-1 copy from phage library containing collation of known sequences of proteins and peptides from the EMBL collection. This database was created by the European Bioinformatics Institute, the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and commercial entities requires a license agreement (see http://www.isb-sib.ch/aboutme/a)
SBC	EMBL I26336; AAAS5698.1;
SCE	EMBL; U56725; ADML1466.1; -;
SCC	EMBL; U10149; AAC50076.1; -;
SCD	HSPB; P19120; 3HSQ.
SCE	Genevay HGNC:5235; HSPA2.
SCH	MTM_140560;-;
SCL	InferPro: IPROU1023; Hsp70.
SCT	PhosphoSitePlus:P000089; HSHTSHOCK70.
SDD	Problem: P0000089; HSP70; 1.
SDE	PROSITE; PS00297; HSP70_1; 1-
SDF	PROSITE; PS00329; HSP70_2; 1-
SDB	PROSITE; PS01036; HSP70_3; 1-
SDC	ATP-binding; Chaperone; Heat shock; Multigene family.
SDE	CONFLICT 24 54 MISSING (IN REF. 3);
SDF	LENGTH 266 266 MSISSI 3
SDD	SEQUENCE 639 AA; 70021 MW; 3851f55d4eaf78729 CnCG64;
SDR	Query Match 8.6%; Score 55; DB 1; Length 639;
SDS	Best Local Similarity 100.0%; Pred.No. 2.4e-47;
SDT	Matches 55; Conservative 0; Mismatches 0; Indels 0; Caps 0;
OEY	6 ATCIDLGTTTCGVGFQRNGVEIIIDAGCSKRTPSYVAFETRELIDAAKNQA 60
ODB	 7 ALRIDGLGTTCGGVFGRNGVAELIIDAGDSNTITPSYAIVDTIRLLDGAKNQVA 61
RESULT 14	
ID ID HS73_RAT	STANDARD: PROT; 641 AA.
AC RS5063;	
DZ 01-OCT-1996 (rel. 34; Created)	
DR 01-OCT-1996 (rel. 34; Last annotation update)	
DT 01-OCT-1996 (rel. 34; Last annotation update)	
DE Heat shock 70 kDa protein 3 (HSP70.3). HSP70-3.	
NS Rattus norvegicus (Rat).	

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN 11
 RM SEQUENCE FROM N.A.
 RC MEDLINE=95012453; PubMed=7927536;
 RX Walter L., Raub F., Guenther R.;
 RT Comparative analysis of the three major histocompatibility complex-
 linked heat shock protein 70 (hsp70) genes of the rat.*;
 RL Immunogenetics 40:335-350(1994).
 CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
 CC OTHER PROTEINS AGAINST AGGREGATION AND MEDATE THE FOLDING
 CC OF REVERSELY TRANSLATED PROTEINS.
 CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
 CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF
 CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET
 CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
 CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
 CC -1- INDUCTION: BY HEAT SHOCK.
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X77209; CAA54424.1; -;
 DR HSPB; P08107; 1h30.
 DR DR
 DR InterPro: IPR001023; HSP70.
 DR Pfam: PF00012; HSP70.1
 DR PRINTS: PS00301; HEATSHOCK70.
 DR PROSITE: PS00297; HSP70.1
 DR PROSITE: PS00329; HSP70.1
 DR PROSITE: PS00329; HSP70.2; 1.
 DR PROSITE: PS00329; HSP70.3; 1.
 DR ATP-binding; Chaperone; Heat shock; Multigene family.
 KM SEQUENCE 641 AA; 70549 MW; 8C77AA5F9B9252 CRC64;
 SO
 Query Match 8.6%; Score 55; DB 1; Length 641;
 Best Local Similarity 100.0%; Pred. No. 2; de-47;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 6 AIGIDLGITTSYGVGVHOGKVEIILANDGNNTPSYVAFTDRLRIIGDAKNNOVA 60
 DB 8 AIGIDLGITTSYGVGVHOGKVEIILANDGNNTPSYVAFTDRLRIIGDAKNNOVA 62
 ID HS7L.HUMAN STANDARD; PRT; 641 AA.
 AC P34931; G9UOM1;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Heat shock 70 kDa protein 1-HOM (HSP70-HOM).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN 11
 RM SEQUENCE FROM N.A.
 RC MEDLINE=95035806; PubMed=1700760;
 RX M. Campbell R.D.;
 RT Structure and expression of the three MHC-linked HSP70 genes.*;
 RL Immunogenetics 32:242-251(1990).
 (2)
 RN SEQUENCE FROM N.A.
 RM Roven L., Qin S., Madan A., Dickhoff R., Dots M., Madan A., Hicks P.,

RA Loretz C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.;
 RT "Sequence of the human major histocompatibility complex class III
 RT region".
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN 31
 RM UNISTAT VET-493
 RC MEDLINE=92406261; PubMed=4356099;
 RX Milner C.M., Campbell R.D.;
 RT Polymorphic analysis of the three MHC-linked HSP70 genes.*;
 RL Immunogenetics 36:357-363(1992).
 CC -1- INDUCTION: NOT INDUCED BY HEAT SHOCK.
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
 CC -1- MISCELLANEOUS: ENCODED IN THE MHC-III COMPLEX.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed, usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M59829; AAA63228.1; -;
 DR EMBL: AF134726; A021817.1; -;
 DR PIR: B45871; B45871.
 DR HSPB; P08107; 1h30.
 DR DR
 DR Genew; HGNC:5234; HSPAL1.
 DR MIM: 140539; 001023; HSP70.
 DR PRINTS: PS00301; HEATSHOCK70.
 DR PROSITE: PS00089; HSP70.1
 DR PROSITE: PS00297; HSP70.1
 DR PROSITE: PS00329; HSP70.2; 1.
 DR PROSITE: PS00329; HSP70.3; 1.
 DR ATP-binding; Multigene family; Polymorphism.
 KM VARIANT 493 493
 FT CONFLICT 408 408 V -> A (IN REF. 2).
 FT CONFLICT 424 424 V -> T (IN REF. 2).
 FT SEQUENCE 641 AA; 70399 MW; 5CF758C9CF6E855 CRC64;
 SO
 Query Match 8.6%; Score 55; DB 1; Length 641;
 Best Local Similarity 100.0%; Pred. No. 2; de-47;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 6 AIGIDLGITTSYGVGVHOGKVEIILANDGNNTPSYVAFTDRLRIIGDAKNNOVA 60
 DB 8 AIGIDLGITTSYGVGVHOGKVEIILANDGNNTPSYVAFTDRLRIIGDAKNNOVA 62
 ID HS7L.HUMAN STANDARD; PRT; 641 AA.
 AC P34931; G9UOM1;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Heat shock 70 kDa protein 1-HOM (HSP70-HOM).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN 11
 RM SEQUENCE FROM N.A.
 RC MEDLINE=95035806; PubMed=1700760;
 RX M. Campbell R.D.;
 RT Structure and expression of the three MHC-linked HSP70 genes.*;
 RL Immunogenetics 32:242-251(1990).
 (2)
 RN SEQUENCE FROM N.A.
 RM Roven L., Qin S., Madan A., Dickhoff R., Dots M., Madan A., Hicks P.,

Search completed: December 4, 2002, 16:51:59
 Job Time : 15 secs

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PS Disclosure: Page 19; 77pp; English.

XX proteins AM51319-W54364 are examples of proteins produced in the
CC endosome of the endometrium. The presence and quantities of these proteins
CC can be detected using 2D gel electrophoresis and comparison of cell lysates.
CC The proteins can be used as biochemical markers to detect the phase of
CC the endometrium and can be measured in body fluids, obviating the need
CC for endometrial biopsies.

XX Sequence 641 AA:

Query Match 100.0%; Score 641; DB 19; Length 641;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 1 MKAALIGDGGTTCVCEVGRKVELIANDGQNTPTTSVAFTDERLIGDAKNQVA 60
DB 1 MKAALIGDGGTTCVCEVGRKVELIANDGQNTPTTSVAFTDERLIGDAKNQVA 60
0Y 61 LNDQNTVEDAKRLIGRFEDPVOSMKHPVOYINDGQKRPVOYSKGTAKAFPEEIS 120
DB 61 LNDQNTVEDAKRLIGRFEDPVOSMKHPVOYINDGQKRPVOYSKGTAKAFPEEIS 120
0Y 121 SWVLTMKKEIAENYLGTPVNAVITVPAYFNDSORATKQAGVJAGLAVLNIINEPTAA 180
DB 121 SWVLTMKKEIAENYLGTPVNAVITVPAYFNDSORATKQAGVJAGLAVLNIINEPTAA 180
0Y 181 IAVGLDRGTGKGBRNVLIFDLGGTTPDVSILITLDGCFEYKATAGDTHLGGEDDNRVLNH 240
DB 181 IAVGLDRGTGKGBRNVLIFDLGGTTPDVSILITLDGCFEYKATAGDTHLGGEDDNRVLNH 240
0Y 241 PVEBFKRKKKDISSONKRAVRRLRTACRAKRPRTJSSSTQASLEIDSLFEGIDFTSTTRA 300
DB 241 PVEBFKRKKKDISSONKRAVRRLRTACRAKRPRTJSSSTQASLEIDSLFEGIDFTSTTRA 300
0Y 301 REBELCSDLFSTSLPEPEKALRDAKLIDKQIHDIYVNGSGSTRIPVOKLIDOFFNGRDLN 360
DB 301 REBELCSDLFSTSLPEPEKALRDAKLIDKQIHDIYVNGSGSTRIPVOKLIDOFFNGRDLN 360
0Y 361 KSIIMPDEANVAGAAVOALILMGKSEBNVDLLIDVAFLSLGLETAGGVMTALIKRNSIT 420
DB 361 KSIIMPDEANVAGAAVOALILMGKSEBNVDLLIDVAFLSLGLETAGGVMTALIKRNSIT 420
0Y 421 PTKQTQIIFTTYSNDQPGVLIOVEGGRAMTKNNMLGRELISITPPAPNGVQPIEVTEDI 480
DB 421 PTKQTQIIFTTYSNDQPGVLIOVEGGRAMTKNNMLGRELISITPPAPNGVQPIEVTEDI 480
0Y 481 DANGLILMTAPYSPGCAKNTITQVGBGRAMTKNNMLGRELISITPPAPNGVQPIEVTEDI 540
DB 481 DANGLILMTAPYSPGCAKNTITQVGBGRAMTKNNMLGRELISITPPAPNGVQPIEVTEDI 540
0Y 541 ALESTAFNMKSAVEDDELNGKISBAKKAKYLDAQEVLISMLDANLLEDFEHRKKELE 600
DB 541 ALESTAFNMKSAVEDDELNGKISBAKKAKYLDAQEVLISMLDANLLEDFEHRKKELE 600
0Y 601 QVCNPITISGLYQACGPGFGGAGQPGGASGPPTIEED 641
DB 601 QVCNPITISGLYQACGPGFGGAGQPGGASGPPTIEED 641

RESULT 2

AA023652 AA023652 standard: protein: 641 AA.

AA023652:

DT 05-JAN-2001 (first entry)

XX Human heat shock protein Hsp70.1 protein sequence SEQ ID NO:4.

XX ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;
XX Immune response; infectious disease; malaria; cytokine T cell;

KW cytosolic; immunostimulant; cellular immune response inducer;
KW protozoicide; Leukemia; cancer.

XX Homo sapiens.

XX WO200049041-A1.

XX 24-AUG-2000.

XX 18-FEB-2000; 2000MO-JF00941.

XX 19-FEB-1999; 99JP-0041535.

XX (SUNE) SUMITOMO ELECTRIC IND CO.

XX Shinbara N, Udono H, Yui K;

XX WPT; 2000-543748/49.

XX Fused protein capable of inducing cellular immune response, useful as

XX active ingredient for drug compositions in preventing and/or treating

XX infectious diseases such as malaria or cancer

XX Claim 3: Page 46-48; 72pp; Japanese.

XX The present invention describes a fused protein (1) prepared from a
CC protein having a DNA encoding (1); (2) a drug composition containing (1)
CC cytosolic T cell, and a protein containing the Atpase domain of a heat
CC shock protein. Also described are: (1) a drug composition containing (1)
CC as active ingredient; (2) a DNA encoding (1); (3) an expression vector
CC containing the DNA of (2); and (4) a transformatant which can retain the
CC expression vector of (3). (1) has cytosolic, immunostimulant and
CC protozoicide activities, and can be used as a cellular immune response
CC inducer. (2) is a drug composition for preventing and/or treating
CC compositions in preventing and/or treating infectious diseases such as
CC malaria or cancer e.g., to provide systemic immunity against leukemia.
CC The present sequence represents a specifically claimed heat shock
XX protein for use in a fused protein of the present invention.

XX Sequence 641 AA:

Query Match 100.0%; Score 641; DB 21; Length 641;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 1 MKAALIGDGGTTCVCEVGRKVELIANDGQNTPTTSVAFTDERLIGDAKNQVA 60
DB 1 MKAALIGDGGTTCVCEVGRKVELIANDGQNTPTTSVAFTDERLIGDAKNQVA 60
0Y 61 LNDQNTVEDAKRLIGRFEDPVOSMKHPVOYINDGQKRPVOYSKGTAKAFPEEIS 120
DB 61 LNDQNTVEDAKRLIGRFEDPVOSMKHPVOYINDGQKRPVOYSKGTAKAFPEEIS 120
0Y 121 SWVLTMKKEIAENYLGTPVNAVITVPAYFNDSORATKQAGVJAGLAVLNIINEPTAA 180
DB 121 SWVLTMKKEIAENYLGTPVNAVITVPAYFNDSORATKQAGVJAGLAVLNIINEPTAA 180
0Y 181 IAVGLDRGTGKGBRNVLIFDLGGTTPDVSILITLDGCFEYKATAGDTHLGGEDDNRVLNH 240
DB 181 IAVGLDRGTGKGBRNVLIFDLGGTTPDVSILITLDGCFEYKATAGDTHLGGEDDNRVLNH 240
0Y 241 PVEBFKRKKKDISSONKRAVRRLRTACRAKRPRTJSSSTQASLEIDSLFEGIDFTSTTRA 300
DB 241 PVEBFKRKKKDISSONKRAVRRLRTACRAKRPRTJSSSTQASLEIDSLFEGIDFTSTTRA 300
0Y 301 REBELCSDLFSTSLPEPEKALRDAKLIDKQIHDIYVNGSGSTRIPVOKLIDOFFNGRDLN 360
DB 301 REBELCSDLFSTSLPEPEKALRDAKLIDKQIHDIYVNGSGSTRIPVOKLIDOFFNGRDLN 360
0Y 361 KSIIMPDEANVAGAAVOALILMGKSEBNVDLLIDVAFLSLGLETAGGVMTALIKRNSIT 420
DB 361 KSIIMPDEANVAGAAVOALILMGKSEBNVDLLIDVAFLSLGLETAGGVMTALIKRNSIT 420

XX	
DE	Human heat shock protein Hsp71.
KW	Hsp71; human; heat shock protein; Immunotherapy; therapy; cancer;
KX	Infection; vaccine.
OS	
XN	Hemo sapiens.
XX	
FH	Key
FT	Binding-site
FT	Location/Ovalifiers
FT	391..615
FT	/note-"peptide-binding domain"
FT	Region
FT	395..502
FT	/note-"beta-helix motif"
FT	400..440
FT	/note-"peptide-binding core"
XX	
PN	M0200152791-A2.
XX	
PD	26-JUL-2001.
PD	
PF	18-JAN-2001; 2001WO-US01781.
PF	
PR	20-JAN-2000; 2000US-0488393.
XX	
PA	(UYCO-) UNIV CONNECTICUT HEALTH CENT.
XX	
P1	Srivastava PK;
DR	
MP	WPI; 2001-457506/49.
XX	
PT	Pharmaceutical composition used to treat or prevent infection of
PT	cancer, comprises a complex comprising at least two unrelated
PT	fragment associated with a molecule displaying antigenicity of an
PT	infectious agent or cancer cell -
XX	
P5	Claim 46; Fig 1C; 106pp; English.
XX	
XX	The present sequence is that of human heat shock protein (HSP)
CC	protein an inducible form of a hsp70 family protein. The invention
CC	relates to a peptide fragment of said protein, to a method of
CC	antigenic molecules and their use in immunotherapy for the treatment
CC	of infectious diseases and cancer. Claimed methods of treating or
CC	preventing cancer/infectious disease involve culturing a cancer
CC	cell/infected cell transformed with a nucleic acid encoding a HSP
CC	peptide-binding domain, recovering complexes of the HSP fragments
CC	nona covalently associated with peptides from the cancer cell/infected
CC	cell, and administering the recovered complexes. These methods can
CC	and 400-440 of the binding fragments comprising amino acids 391-615
CC	domain and peptide-binding core.
XX	
XX	Sequence 641 AA;
XQ	

Query Match	Local Similarity	100.0%	Score	64:	DB 22:	Length	64:
Best	Local Similarity	100.0%	Pred. No.:	0:	Mismatches	0:	Indels
Matches	Conservative	0:	Mismatches	0:	Indels	0:	Gaps
Qy	1	MAKALICIDIGCTTCTGCGFQDHGKVEIANDGSKRTTTSYAFIDYRILGDAANOVA	60				
Db	1	MAKALAIQIDITTTCTCTGCGFQDHGKVEIANDGSKRTTTSYAFIDYRILGDAANOVA	60				
Qy	61	LNPNQNVEDAKLLGKRRGQDPVVGSDKIMPFQVYINQCGKPPVQVSGSTATAYEELS	120				
Db	61	LNPNQNVEDAKLLGKRRGQDPVVGSDKIMPFQVYINQCGKPPVQVSGSTATAYEELS	120				
Qy	121	SMPLTRKKEIAENLCGPTPNNAVITPAIFPDSQKATADGAYAGLNLKRIEFTAA	180				
Db	121	SMPLTRKKEIAENLCGPTPNNAVITPAIFPDSQKATADGAYAGLNLKRIEFTAA	180				
Qy	181	IANGDRIRNGSRNVLITDGGGFPDVSILTIIDQITFEYKATAGDTHLGGEOPFNRLVNH	240				
Db	181	IANGDRIRNGSRNVLITDGGGFPDVSILTIIDQITFEYKATAGDTHLGGEOPFNRLVNH	240				

Oy	241	EYEFERKHNKKIOXKQKPAVRRLTACAPAKFPLSSSTOASLSEIOLPESIDPTSTR	300
Oy	242	EVEFERKHKKIOXKQKPAVRRLTACAPAKFPLSSSTOASLSEIOLPESIDPTSTR	300
Oy	243	EVEFERKHKKIOXKQKPAVRRLTACAPAKFPLSSSTOASLSEIOLPESIDPTSTR	300
Dy	301	REBELCDLSFLSTLEVERALADKAADKRAKDLDLYLVGSGSRIPRYOKLLDFFNGRDLN	360
Dy	302	REBELCDLSFLSTLEVERALADKAADKRAKDLDLYLVGSGSRIPRYOKLLDFFNGRDLN	360
Dy	303	REBELCDLSFLSTLEVERALADKAADKRAKDLDLYLVGSGSRIPRYOKLLDFFNGRDLN	360
Oy	361	KSNPEDEAVAGAAVOAAILMGDSERNVDLLILVPAPISLGLETAGVFTALLIKRNSTI	420
Oy	362	KSNPEDEAVAGAAVOAAILMGDSERNVDLLILVPAPISLGLETAGVFTALLIKRNSTI	420
Dy	481	DANGILNVATVKTSCKANKITITDKGLSKSEETERNVOAEKKAEDVOREVSARK	540
Oy	541	ALNSTAFNMKSVADEBCLAKISENDKKRVLCQCEYISMIDANTLLAKODEEHRKEELE	600
Dy	542	ALNSTAFNMKSVADEBCLAKISENDKKRVLCQCEYISMIDANTLLAKODEEHRKEELE	600
Oy	601	GVCPNPISIGLYGAGCGPGSCGAGPKGSAGSGETTEVP	641
Dy	602	GVCPNPISIGLYGAGCGPGSCGAGPKGSAGSGETTEVP	641
Dy	603	GVCPNPISIGLYGAGCGPGSCGAGPKGSAGSGETTEVP	641
Dy	604	GVCPNPISIGLYGAGCGPGSCGAGPKGSAGSGETTEVP	641
ID	AAB23252	standard: Protein; 624 AA.	
PD	AAB23252		
AC	AAB23252:		
DF	29-JAN-2001	(first entry)	
DE	Human Hsp72	(heat shock protein 72).	
Xx	Human Hsp72: heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor;		
Kw	expression modulator; JNK phosphatase inhibitor; antiproliferative;		
Kw	dnaJ screening; cancer; leukemia; lymphoma; solid tumour; sarcoma;		
Kw	cardioma; breast cancer; prostate cancer; premalignant condition.		
Xx	Homo sapiens.		
Xx	Mo200054814-NL.		
PN	21-SEP-2000.		
PD	17-MAR-2000; 2000MO-DU07350.		
FE	16-MAR-1999; 9905-O125046.		
PX	(PHLT-) PHYLOGENY INC.		
PA	Vollloch VZ, Sherman M:		
PI	WPI: 2000-647056/62.		
DR	R-FSDBI: AAB97541.		
XX	Identifying compounds that inhibit proliferation of cells and capable		
PT	of modulating the expression of heat shock protein 72 gene and/or		
PT	activity of Hsp72 useful for treating cancers such as leukemia,		
PT	lymphoma -		
XX	Examples: Fig 16b: 77pp: English.		
PS	The invention relates to a novel method of identifying compounds that		
Cc	inhibit proliferation of cells comprising contacting a test compound with		
Cc	a cell which overexpresses Hsp72 (heat shock protein 72), and determining		
Cc	if the test compound inhibits activity or expression of Hsp72.		
Cc	optionally, Hsp72 is contacted with the test compound under optimum		

CC conditions to allow the two components to interact and bind, forming a
 CC complex which is detected. The invention also relates to a method of
 CC identifying compounds that inhibit Hsp72-mediated JNK phosphatase
 CC activation, comprising contacting a test compound with a cell which
 CC expresses Hsp72, exposing the cell to a heat induced stress, and
 CC measuring the amount of JNK phosphatase activity. The amount of
 CC JNK phosphatase activity is measured by measuring the amount of
 CC inhibitor of Hsp72 or JNK phosphatase activity. The compounds identified as
 CC inhibitors of Hsp72 or JNK phosphatase activity are useful for
 CC inhibiting the proliferation of cells. Modulation of the activity of the
 CC JNK phosphatase or Hsp72 is used to treat a proliferative disorder such
 CC as cancers (e.g., leukemia, lymphoma, solid tumours such as sarcomas and
 CC carcinomas, breast cancer, prostate cancer). The compounds that inhibit
 CC Hsp72 or JNK phosphatase activity also prevent significant conditions
 CC associated with the progression of a neoplastic or malignant disease
 CC and to prevent progression to a neoplastic or malignant disease in a patient
 CC compounds that inhibit Hsp72 function are administered to a patient
 CC having a disease or disorder mediated by an increase of Hsp72 expression
 CC or actively relative to normal levels. The present sequence represents
 CC human Hsp72 used in the exemplifications of the invention.

XX Sequence 624 AA:

Query Match 97.3% Score 624: DB 21: Length 624:
 Best Local Similarity 100.0%: Pred. No. 0:
 Matches 624: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

0Y 1 MAAAAAGTGGTATTCVGVFGHKEKELIANDGKRTTSTVAFDTFERLIGDAAKNOYA 60
 DB 1 MAAAAAGTGGTATTCVGVFGHKEKELIANDGKRTTSTVAFDTFERLIGDAAKNOYA 60
 0Y 61 LNPQTVFAKRLIGKRPVQVDSMKHMPFQVNDGKRPVQVSGTAKAYFEIS 120
 DB 61 LNPQTVFAKRLIGKRPVQVDSMKHMPFQVNDGKRPVQVSGTAKAYFEIS 120
 0Y 121 SMVLTKKEELAEAYLGPTNATVTPAVPNDGKRTTSDGAGVLAAGLVIETPTAA 180
 DB 121 SMVLTKKEELAEAYLGPTNATVTPAVPNDGKRTTSDGAGVLAAGLVIETPTAA 180
 0Y 181 IAVGLDPTGKGRNVLEFDGGTFPVSLTIDDIPEYKATAGDTHLGGEFNPVLNH 240
 DB 181 IAVGLDPTGKGRNVLEFDGGTFPVSLTIDDIPEYKATAGDTHLGGEFNPVLNH 240
 0Y 241 PVEERKRRKIDISQNKRAVRLKACERAKRTSSSTGASLETDSLEFGIDPTYSITRA 300
 DB 241 PVEERKRRKIDISQNKRAVRLKACERAKRTSSSTGASLETDSLEFGIDPTYSITRA 300
 0Y 301 REFELSDLFSTLPEPERKALDKAKQIHVLVLGSGSRIPYKOKLADGPFNRDIN 360
 DB 301 REFELSDLFSTLPEPERKALDKAKQIHVLVLGSGSRIPYKOKLADGPFNRDIN 360
 0Y 361 KSTNDEAVANGAQAALIMKDSSENODILLIDVAPLSGLIETNAGVWALIKRSTT 420
 DB 361 KSTNDEAVANGAQAALIMKDSSENODILLIDVAPLSGLIETNAGVWALIKRSTT 420
 0Y 421 PTGQTOLETTYSDNPGVLIQVYEGEAMRKDNMLTARELSGTPAPARKVQLETTEDI 480
 DB 421 PTGQTOLETTYSDNPGVLIQVYEGEAMRKDNMLTARELSGTPAPARKVQLETTEDI 480
 0Y 481 DANGLIANTATDSTGAKNTITTNKGRLSKEELERWQAEKRYAKDEQVERVSAN 540
 DB 481 DANGLIANTATDSTGAKNTITTNKGRLSKEELERWQAEKRYAKDEQVERVSAN 540
 0Y 541 ALESYAVNKKSAVEDGLKRLISEAKRKVYLDCOEYISMLDNLTAJKEKEFEKKEKE 600
 DB 541 ALESYAVNKKSAVEDGLKRLISEAKRKVYLDCOEYISMLDNLTAJKEKEFEKKEKE 600
 0Y 601 QVNCPIISGLIQAGGPGPGGGA 624
 DB 601 QVNCPIISGLIQAGGPGPGGGA 624

RESULT 6
 AAB23653

ID AAB23653 standard; protein; 640 AA.

XX AAB23653:

AC 05-JAN-2001 (first entry)

DT Human heat shock protein Hsp70 protein sequence SEQ ID NO:5.

KW ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;

KW Immune response; Infectious disease; malaria; cytotoxic T cell;

KW Cytotoxic; Immunostimulant; cellular immune response inducer;

KW protozoacide; leukemia; cancer.

XX Homo sapiens.

XX NC0200049041.A1.

PD 24-NOV-2000.

XX 18-FEB-2000: 2000MO-JP00941.

XX 19-FEB-1999: 99JP-0041535.

XX (SIME) SUMITOMO ELECTRIC IND CO.

XX Shinbara N, Udono H, Yui K;

XX WPI: 2000-543748/49.

XX Fused protein capable of inducing cellular immune response, useful as

XX active ingredient for drug or vaccine for preventing and/or treating

XX infectious diseases such as malaria or cancer

XX Claim 3: Page 49-52: 72pp: Japanese.

XX The present invention describes a fused protein (1) prepared from a
 CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by
 CC CTLs, and a protein (2) containing the amino acid sequence of the
 CC shock protein. Also described are (1) a protein composition containing (1)
 CC as active ingredient; (2) a DNA encoding (1); (3) an expression vector
 CC containing the DNA of (2); and (4) a transformant which can retain the
 CC expression vector of (3). (1) has cytotoxic, immunostimulant and
 CC protozoacide activities, and can be used as a cellular immune response
 CC inducer. The protein is useful as an active ingredient for drug
 CC compositions in preventing and/or treating infectious diseases such as
 CC malaria, and as an active ingredient for vaccine compositions for
 CC preventing and/or treating infectious diseases such as malaria.
 CC The present sequence represents a specifically claimed heat shock
 CC protein for use in a fused protein of the present invention.

XX Sequence 640 AA:

Query Match 99.3% Score 412: DB 21: Length 640:
 Best Local Similarity 99.3%: Pred. No. 0:
 Matches 632: Conservative 0: Mismatches 1: Indels 1: Gaps 1:

0Y 8 GIDLTITSCVGVFGHKEKELIANDGKRTTSTVAFDTFERLIGDAAKNOYALNPQTV 67
 DB 8 GIDLTITSCVGVFGHKEKELIANDGKRTTSTVAFDTFERLIGDAAKNOYALNPQTV 67
 0Y 67 FDKAKLIGKRPVQVDSMKHMPFQVNDGKRPVQVSGTAKAYFEIS 127
 DB 67 FDKAKLIGKRPVQVDSMKHMPFQVNDGKRPVQVSGTAKAYFEIS 127
 0Y 127 KETLAELATYCPVNTAVTPAVPNDGKRTTSDGAGVLAAGLVIETPTAAIAYGLDR 187
 DB 127 KETLAELATYCPVNTAVTPAVPNDGKRTTSDGAGVLAAGLVIETPTAAIAYGLDR 187
 0Y 187 TKGGRNVLEFDGGTFPVSLTIDDIPEYKATAGDTHLGGEFNPVLNHVVEERK 247
 DB 187 TKGGRNVLEFDGGTFPVSLTIDDIPEYKATAGDTHLGGEFNPVLNHVVEERK 247
 0Y 247 TKGGRNVLEFDGGTFPVSLTIDDIPEYKATAGDTHLGGEFNPVLNHVVEERK 247
 DB 247 TKGGRNVLEFDGGTFPVSLTIDDIPEYKATAGDTHLGGEFNPVLNHVVEERK 247
 0Y 248 KHKKIDISQNKRAVRLKACERAKRTSSSTGASLETDSLEFGIDPTYSITRAFEELCS 307
 DB 248 KHKKIDISQNKRAVRLKACERAKRTSSSTGASLETDSLEFGIDPTYSITRAFEELCS 307

```

Db      248 KKKKDIISNKKAVRRLTACRRKATLSSSTQASLLETLSFEGIDPFTSITRRAREELCS 307
Oy      308 DLFSTLSPVKAALNDKAIIDKAQIHDIYLVGSGTRIPRYOKILIDPFNGRDLMKSNIPDE 367
Db      308 DLFSTLSPVKAALNDKAIIDKAQIHDIYLVGSGTRIPRYOKILIDPFNGRDLMKSNIPDE 367
Oy      368 AVAAGAAVOAAILMDGKSENVDLLIDVAPJLSGLETAGVWFLAKNSSTLPTKOTQI 427
Db      368 AVAAGAAVOAAILMDGKSENVDLLIDVAPJLSGLETAGVWFLAKNSSTLPTKOTQI 427
Oy      428 PTTTSDNOCVLIQVYEGBRANKDNMLGRRELSTGIPAPKCVQI EYVTDIDANGILM 487
Db      428 PTTTSDNOCVLIQVYEGBRANKDNMLGRRELSTGIPAPKCVQI EYVTDIDANGILM 486
Oy      488 VTATDSSTGKANKITITNKGRLSKLEEIVQVQAEKKAEDVORBRYSAKNALESYAF 547
Db      487 VTATDSSTGKANKITITNKGRLSKLEEIVQVQAEKKAEDVORBRYSAKNALESYAF 546
Oy      548 NKKANAVDEBGLKKGITSAQKKKYLKCEVTSIDANTLAANDPEHKKKELQVCNPIT 607
Db      547 NKKANAVDEBGLKKGITSAQKKKYLKCEVTSIDANTLAANDPEHKKKELQVCNPIT 606
Oy      608 SGLVYAGAGPQGGAGQPGKSGSGPTEIEVD 641
Db      607 SGLVYAGAGPQGGAGQPGKSGSGPTEIEVD 640

RESULT 7
AA58409
- ID      AAVB8409 standard; Protein: 554 AA.
XX
XX      AAVB8409:
XX      31-JUL-2000 (first entry)
XX
DE      Human heat shock protein SHSP70 amino acid sequence.
XX
XX      Human: heat shock protein: HSP70; chromosome 6p21.3-22; stress;
XX      chromosome 14q22-24; transcription; rheumatism; schizophrenia;
XX      depression; nephrotic syndrome; SHSP70.
XX      Homo sapiens.
XX      JF2000069999-A.
XX
PD      07-MAR-2000.
XX
PE      01-JUN-1995. 99JP-0257146.
XX
PR      01-JUN-1995. 95JP-0158581.
XX
PA      (HOKEN-) HOKEN KAKAKU KENKYUSHO KK.
XX
DR      WPI: 2000-264458/23.
XX      N-PSDB: AAA15621.
XX
PT      Abnormal transcription of intron211, HSP70mRNA under acute and
XX      chronic continuous load of stress in a human being and its application
XX      Examples: Fig 2; 11pp; Japanese.
XX
XX      This sequence represents the human heat shock protein SHSP70 amino acid
XX      sequence. Human heat shock proteins are located on chromosomes 6p21.3-22
XX      and 14q22-24. The abnormal transcription of
XX      intron211, HSP70mRNA under acute and
XX      chronic continuous load of stress in a human being and its improvement of
XX      the abnormal transcription of HSP70 can be used in the improvement of
XX      stress and response and diagnosis of stress diseases including
XX      rheumatism, schizophrenia, depression and nephrotic syndrome.
XX
SQ      Sequence 554 AA.
Query Match 1 52.0%; Score 333; Db 21; Length 554;

```

```

Best Local Similarity 99.6%; Pred. No. 2,3e-313;
Matches 553; Conservative 0; Mismatches 1; Idels 1; Gaps 1;
Oy      87 MKMPRPQVLI NQDQKRVQSKSGKFAFYRELSISWYLTWKELIARAYIGVPTNAIVTY 146
Db      1 MKMPRPQVLI NQDQKRVQSKSGKFAFYRELSISWYLTWKELIARAYIGVPTNAIVTY 60
Oy      147 PAFVNSORATKADGVIAGLNLVRIINEPTAAIAVGLDTGKGERNYLIFPLGGSTPD 206
Db      61 PAFVNSORATKADGVIAGLNLVRIINEPTAAIAVGLDTGKGERNYLIFPLGGSTPD 120
Oy      207 VSGLITDQCTFPRKATAGCTGLGCEPDNLVNFYEEFKKKKKKDIISNKKAVRRLRFLTA 266
Db      121 VSGLITDQCTFPRKATAGCTGLGCEPDNLVNFYEEFKKKKKKDIISNKKAVRRLRFLTA 180
Oy      267 CRRKRTLSSTQASLLETLSFEGIDPFTSITRRAREELCSDFSTLSPVKAALNDKAI 326
Db      181 CRRKRTLSSTQASLLETLSFEGIDPFTSITRRAREELCSDFSTLSPVKAALNDKAI 240
Oy      327 DKAQIHDIYLVGSGTRIPRYOKILIDPFNGRDLMKSNIPDEAVYGAOVAAILMDGKSE 386
Db      241 DKAQIHDIYLVGSGTRIPRYOKILIDPFNGRDLMKSNIPDEAVYGAOVAAILMDGKSE 300
Oy      387 NVQVOLLIDVAPJLSGLETAGVWFLAKNSSTLPTKOTQIPTTSDNOCVLIQVYEGE 446
Db      301 NVQVOLLIDVAPJLSGLETAGVWFLAKNSSTLPTKOTQIPTTSDNOCVLIQVYEGE 360
Oy      447 PAMTRKDNMLGRRELSTGIPAPKCVQI EYVTDIDANGILMVTATDSSTGKANKITITND 506
Db      361 PAMTRKDNMLGRRELSTGIPAPKCVQI EYVTDIDANGILMVTATDSSTGKANKITITND 419
Oy      507 KGRLSKEETIERBVQAEKTKAEDVORBRYSAKNALESYAFANNKSAVEDGLAKGISPAD 566
Db      420 KGRLSKEETIERBVQAEKTKAEDVORBRYSAKNALESYAFANNKSAVEDGLAKGISPAD 479
Oy      567 KKKYLVKCEVTSIDANTLAANDPEHKKKELQVCNPITISGLYQAGAGPQGGAGQ 626
Db      480 KKKYLVKCEVTSIDANTLAANDPEHKKKELQVCNPITISGLYQAGAGPQGGAGQ 539
Oy      627 PGGSGSGPTEIEVD 641
Db      540 PGGSGSGPTEIEVD 554

RESULT 8
AA58410
- ID      AAVB8410 standard; Protein: 554 AA.
XX
XX      AAVB8410:
XX      31-JUL-2000 (first entry)
XX
DE      Human heat shock protein SHSP70 amino acid sequence.
XX
XX      Human: heat shock protein: HSP70; chromosome 6p21.3-22; stress;
XX      chromosome 14q22-24; transcription; rheumatism; schizophrenia;
XX      depression; nephrotic syndrome; SHSP70.
XX      Homo sapiens.
XX      JF2000069999-A.
XX
PD      07-MAR-2000.
XX
PE      01-JUN-1995. 99JP-0257146.
XX
PR      01-JUN-1995. 95JP-0158581.
XX
PA      (HOKEN-) HOKEN KAKAKU KENKYUSHO KK.
XX
DR      WPI: 2000-264458/23.
XX      N-PSDB: AAA15622.
XX

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PN JP2000069999-A.
 PD 07-MAR-2000.
 PK 01-JUN-1995: 99JP-0257146.
 XX 01-JUN-1995: 95JP-0158581.
 PR (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
 XX
 PA WPI: 2000-264458/23.
 DR N-F50B: AAA15620.
 XX
 PF Abnormal transcription of intracellular Hsp70mRNA under acute and
 PT chronic continuous load of stress in a human being and its application
 PS
 PS Claim 2: Fig 1: 11pp: Japanese.
 XX
 XX This sequence represents the human heat shock protein Hsp70 amino acid
 CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22
 CC and 14q22-24. The invention relates to the abnormal transcription of
 CC intracellular Hsp70mRNA under acute and chronic stress load in a human.
 CC The abnormal transcription of Hsp70 can be used in the improvement of
 CC stress and response and diagnosis of stress diseases including
 CC rheumatism, schizophrenia, depression and nephrotic syndrome.
 SS
 SS Sequence 640 AA:
 50
 * Query Match 40.7%: Score 261: DB 21: Length 640:
 Best Local Similarity 99.7%: Pred. No. 1.3e-243:
 Matches 361: Conservative 0: Mismatches 1: Indels 0: Gaps 0:
 Oy 8 GIDGTTSCYGVPOHAKVEIIANOQKRTPTVAFTDRLICDAAANQVALMPOHY 67
 Db 8 GIDGTTSCYGVPOHAKVEIIANOQKRTPTVAFTDRLICDAAANQVALMPOHY 67
 Oy 68 PAAKRLIGKFGDPVVOQDKHNPQVINDGDKKQVQYKGETKAPYEESISAWLTKM 127
 Db 68 PAAKRLIGKFGDPVVOQDKHNPQVINDGDKKQVQYKGETKAPYEESISAWLTKM 127
 Oy 128 KEIENKLGCPYNNNAVITWRATFNDSORNTQKQYVAGLVATINETPMAALVGLDR 187
 Db 128 KEIENKLGCPYNNNAVITWRATFNDSORNTQKQYVAGLVATINETPMAALVGLDR 187
 Oy 188 TCKERNVLIPIIDLGSGFPVSLITIDDIIEVKAETAGDHLGDEDFDNLVNHVEEKK 247
 Db 188 TCKERNVLIPIIDLGSGFPVSLITIDDIIEVKAETAGDHLGDEDFDNLVNHVEEKK 247
 Oy 248 KKKKSDISKRAVRLKTCGRAPKRLSSSTQASLEISLFGIDETYSITRAFEELCS 307
 Db 248 KKKKSDISKRAVRLKTCGRAPKRLSSSTQASLEISLFGIDETYSITRAFEELCS 307
 Oy 308 DLFSGTSLFPEVKALADKAQAHQHLVLDVGGSTRPKVQGLDQFFNDRLLKNSINPDE 367
 Db 308 DLFSGTSLFPEVKALADKAQAHQHLVLDVGGSTRPKVQGLDQFFNDRLLKNSINPDE 367
 Oy 368 AV 369
 Db 368 AV 369
 RESULT 11
 AAR09886
 XX AAR09886 standard; protein: 244 AA.
 AC AAR09886:
 XX
 DT 06-NOV-2000 (first entry)
 XX
 DE Hsp70 C-terminal 244 amino acid polypeptide sequence.
 XX
 KM Heat shock protein 70: Hsp70; NF-kappaB; transplant rejection;

KM autoimmune disease; inflammatory disease; cancer; vascular disease.
 OS Homo sapiens.
 XX W020003113-A1.
 XX
 PD 02-JUN-2000.
 XX
 PF 17-NOV-1999: 99WO-US27244.
 XX
 XX 24-NOV-1998: 98US-0109872.
 PR (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 XX Fujihara SM, Nadler SG:
 PT
 PS WPI: 2000-400029/34.
 DR
 XX Intracellular targeted delivery of compounds using the 70 kilodalton
 PF protein of the heat shock response for the treatment of transplant rejection,
 PT autoimmune diseases and cancer
 PS
 PS Claim 6: Page 17: 31pp: English.
 XX
 XX The present sequence is the C-terminal 244 amino acids of the 70kd heat
 CC shock protein (Hsp70). This sequence was used in a fusion protein with
 CC the p30 subunit of transcription factor NF-kappaB. The sequence which is
 CC not given. This fusion protein was created in order to determine the
 CC ability of the Hsp70 sequence to direct other proteins into the cell. It
 CC was shown that Hsp70 fragments are able to direct other proteins into
 CC the cell, a feature which can be used in the treatment of transplant
 CC rejection, autoimmune diseases such as rheumatoid arthritis, multiple
 CC sclerosis, diabetes, asthma, inflammatory bowel disease, psoriasis,
 CC osteoarthritis, pancreatitis and adult respiratory distress syndrome,
 CC cancer, vascular diseases (such as stenosis and atherosclerosis) and
 CC DNA and RNA viral replication diseases (including herpes).
 SS
 SS Sequence 244 AA:
 50
 * Query Match 38.1%: Score 244: DB 21: Length 244:
 Best Local Similarity 100.0%: Pred. No. 1.0e-227:
 Matches 244: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 Oy 398 PLSLGLETAGCVFALIKKNSITFTKQTOIFTYSDNPGVGLIQVYGERAMTKNNILG 457
 Db 1 PLSLGLETAGCVFALIKKNSITFTKQTOIFTYSDNPGVGLIQVYGERAMTKNNILG 60
 Oy 458 REEISGIPAPRGVPOLEYETPDIDANGILMAYADSGKANKITINRGKRSFEETFR 517
 Db 61 REEISGIPAPRGVPOLEYETPDIDANGILMAYADSGKANKITINRGKRSFEETFR 120
 Oy 518 MVOAKKRYKADDEVQREKRSKNAALNESAFAVEDEGLKQKISBAQKRYLDRQCEY 577
 Db 121 MVOAKKRYKADDEVQREKRSKNAALNESAFAVEDEGLKQKISBAQKRYLDRQCEY 180
 Oy 578 ISMDANLTLAEKDEPRKREKRELEQVYCNIIISGLYQAGAGCPGCGAGCGCSGSGPTI 637
 Db 181 ISMDANLTLAEKDEPRKREKRELEQVYCNIIISGLYQAGAGCPGCGAGCGCSGSGPTI 240
 Oy 638 EEVD 641
 Db 241 EEVD 244
 RESULT 12
 AAR03929
 ID AAR03929 standard; protein: 640 AA.
 AC AAR03929:
 XX
 DT 30-NOV-1990 (first entry)

CC rapid production of functional information from genomic sequence. The
 CC present sequence is a peptide encoded by a single exon nucleic acid
 CC probe of the invention. The present sequence is a peptide encoded by a
 CC single exon nucleic acid probe of the invention. The present sequence is a
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct-sequences.

XX Sequence 168 Aa:

50 Query Match 26.2%; Score 168; DB 22; Length 168;
 Best Local Similarity 100.0%; Pred. No. 4.4e-154;

Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 IEVTFDIDANGIIINVTATKSTGKAKITTTNDKGRSLKEIEIRNVOEAKRYAEDVOR 533

DB 1 IEVTFDIDANGIIINVTATKSTGKAKITTTNDKGRSLKEIEIRNVOEAKRYAEDVOR 60

QY 534 EVSNKMALESYAFPMKSAVEDBGLKGISEADKKKVIYDKOCQEVISMLANTLAKEDEFF 593

DB 61 EVSNKMALESYAFPMKSAVEDBGLKGISEADKKKVIYDKOCQEVISMLANTLAKEDEFF 120

QY 594 HRRKELEYQCNPIISGLYOGAGRGFGGFCGAGRGSGSGSPTEIYVD 641

DB 121 HRRKELEYQCNPIISGLYOGAGRGFGGFCGAGRGSGSGSPTEIYVD 168

RESULT 14

ABR35536

ID ABR35536 standard; Peptide; 168 Aa.

AC ABR35536;

XX 04-FEB-2002 (first entry)

DE Peptide #3042 encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.

OS Homo sapiens.

XX WO200157277-A2.

XX 30-JAN-2001; 2001WO-US00669.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 00-JUN-2000; 2000US-0603408.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0234687.

XX 04-OCT-2000; 2000GB-0024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-48344/752.

PT Human genome-derived single exon nucleic acid probes useful for

XX analyzing gene expression in human foetal liver -

XX Claim 27: SEQ ID NO 28171; 639PP + sequence listing; English.

CC The invention relates to a single exon nucleic acid probe for

CC measuring gene expression in a sample derived from human foetal

CC liver. The single exon nucleic acid probes may be used for predicting,

CC measuring and displaying gene expression in samples derived from human

CC foetal liver. The present sequence is a peptide encoded by a single exon

CC nucleic acid probe of the invention.

CC Note: The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/published_pct-sequences.

XX Sequence 168 Aa:

50 Query Match 26.2%; Score 168; DB 22; Length 168;

Best Local Similarity 100.0%; Pred. No. 4.4e-154;

Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 IEVTFDIDANGIIINVTATKSTGKAKITTTNDKGRSLKEIEIRNVOEAKRYAEDVOR 533

DB 1 IEVTFDIDANGIIINVTATKSTGKAKITTTNDKGRSLKEIEIRNVOEAKRYAEDVOR 60

QY 534 EVSNKMALESYAFPMKSAVEDBGLKGISEADKKKVIYDKOCQEVISMLANTLAKEDEFF 593

DB 61 EVSNKMALESYAFPMKSAVEDBGLKGISEADKKKVIYDKOCQEVISMLANTLAKEDEFF 120

QY 594 HRRKELEYQCNPIISGLYOGAGRGFGGFCGAGRGSGSGSPTEIYVD 641

DB 121 HRRKELEYQCNPIISGLYOGAGRGFGGFCGAGRGSGSGSPTEIYVD 168

RESULT 15

ABR20960

ID ABR20960 standard; Protein; 168 Aa.

AC ABR20960;

XX 23-JUN-2002 (first entry)

DE Protein #2959 encoded by probe for measuring heart cell gene expression.

XX Human; gene expression; heart; microarray; vascular system;

XX cardiovascular disease; hypertension; cardiac arrhythmia;

XX congenital heart disease.

OS Homo sapiens.

XX WO200157274-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00666.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0603408.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0234687.

XX 04-OCT-2000; 2000GB-0024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-48889/53.

PT Single exon nucleic acid probes for analyzing gene expression in human

XX Claim 15: SEQ ID NO 22730; 530PP; English.

CC The present invention relates to single exon nucleic acid probes for

CC measuring human gene expression in a sample derived from human heart (see

CC ABR21355-ABM41305). The present sequence is a protein encoded by one such

CC probe. The probes may be used for predicting, measuring and displaying

CC gene expression in samples derived from human heart. The present sequence

CC is a peptide encoded by a single exon nucleic acid probe of the invention.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO


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CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 168 AA:
Query Match 36 24: Score 168: DB 23: Length 168:
Best Local Similarity 100.0%: Read No 4 4e-154:
Matches 168: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
OY 474 IEVTEDIDANGILNVTATDEKSTGKANKITINDKGRLSKEELBHWQAEKTKAEDEVQR 533
DB 1 IEVTEDIDANGILNVTATDEKSTGKANKITINDKGRLSKEELBHWQAEKTKAEDEVQR 60
OY 534 ERSAXKALLESYAFNNKSAVEDEGLKGISPDKKKYLTXCOEYISMLDNTLAEKDEFE 593
DB 61 ERSAXKALLESYAFNNKSAVEDEGLKGISPDKKKYLTXCOEYISMLDNTLAEKDEFE 120
OY 594 HKRKELEQVCNPIISGLYQAGGPGPGFAGQPGGSGSGSPPTIEVD 641
DB 121 HKRKELEQVCNPIISGLYQAGGPGPGFAGQPGGSGSGSPPTIEVD 168

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Job time : 41 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: December 4, 2002, 16:35:27 : Search time 39 seconds
(Without alignments)
2190.094 Million cell updates/sec

File: us-09-646-835-1

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Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database: A: Geneseq, 101002.*

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- 13: /SID82/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
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- 16: /SID82/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
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- 19: /SID82/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SID82/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SID82/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SID82/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SID82/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3263	100.0	641	19	AAW54349	Human heat shock 7
2	3263	100.0	641	21	AAW23652	Human heat shock 7
3	3263	100.0	641	22	AAW12966	Human heat shock 7
4	3263	100.0	641	22	AAW23534	Human heat shock 7
5	3242	99.0	641	22	AAW10065	Human heat shock 7
6	3229.5	99.0	640	18	AAW84408	Human heat shock 7
7	3229.5	99.0	640	11	AAW03929	Human heat shock 7
8	3211	98.4	640	11	AAW32352	Human heat shock 7
9	3172	97.2	624	14	AAW33004	Human heat shock 7
10	3130	95.9	641	14	AAW33004	Human heat shock 7

11	3125.5	95.8	642	21	AAW23650	Rat heat shock pro
12	3093.5	94.8	640	21	AAW84411	Human heat shock p
13	2862.5	87.7	646	20	AAW17408	Mouse heat shock c
14	2862.5	87.7	646	21	AAW23649	Mouse heat shock p
15	2859.5	87.6	646	19	AAW54364	Heat shock cognate
16	2859.5	87.6	646	19	AAW23657	Human heat shock c
17	2859.5	87.6	646	22	AAW12967	Human heat shock c
18	2859.5	87.6	646	22	AAW12967	Human heat shock c
19	2859.5	87.6	646	22	AAW23655	Human heat shock p
20	2859.5	87.6	646	23	AAW51502	Heat shock protein
21	2859.5	87.6	646	23	AAW23938	GFP-HSC70 fusion p
22	2837.5	87.0	646	11	AAW03927	Rat HSP (hsc70)
23	2837.5	86.5	647	11	AAW03928	Xenopus laevis HSP
24	2837.5	86.5	647	11	AAW03928	Xenopus laevis HSP
25	2803.5	85.9	554	21	AAW84410	Human heat shock p
26	2754.5	84.4	633	14	AAW30002	Mouse SIRT1 homolo
27	2747.5	84.2	634	11	AAW03932	Gallus gallus HSP
28	2747.5	84.2	634	23	AAW848711	Human schizophr
29	2740	84.0	665	21	AAW8386	Lung cancer associ
30	2737	83.9	651	22	AAW60514	Drosophila melanog
31	2692.5	83.3	543	28	AAW24895	Marine bacteri
32	2692.5	83.3	543	28	AAW24895	Marine bacteri
33	2664	81.6	641	22	AAW17708	Drosophila melanog
34	2661.5	81.6	554	21	AAW84412	Human heat shock p
35	2524.5	77.4	620	11	AAW03932	Serratia marcescen
36	2502.5	76.7	656	18	AAW01658	Candida albicans h
37	2455.5	75.6	646	21	AAW53604	Arabidopsis thalia
38	2439.5	74.8	629	22	AAW82209	Drosophila melanog
39	2436.5	74.7	635	12	AAW61525	Drosophila melanog
40	2436.5	74.7	635	12	AAW61525	Drosophila melanog
41	2414.5	74.0	647	20	AAW11380	T. gondii antigen
42	2414.5	74.0	647	22	AAW49099	Toxoplasma gondii
43	2402	73.6	677	11	AAW09418	Hsp70 antigen from
44	2380.5	73.2	676	9	AAW80088	Sequence of 70kd p
45	2386.5	73.1	623	21	AAW53605	Arabidopsis thalia

ALIGNMENTS

RESULT 1	AAW54349	standard; protein: 641 AA.
ID	AAW54349	
XX	AAW54349:	
XX	14-AUG-1998	(first entry)
DE	Human heat shock 70 kd protein 1.	
KW	Endometrium; hyperplasia; adenocarcinoma; proliferative phase;	
KX	2D gel electrophoresis; detection.	
XX	Homo sapiens.	
XX	W09810291.AI.	
PD	12-MAR-1998.	
XX	05-SEP-1997:	97MO-GB02394.
XX	08-APR-1997:	97GB-0007132.
PR	06-SEP-1996:	96GB-0018600.
XX	(CLIN-) CENT CLINICAL & BASIC RES.	
PA	Byrjalsen I, Fey SJ, Larsen P:	
PI	WPI: 1998-207057/18.	
XX	Biochemical markers of human endometrium - useful for, e.g.	
PT	diagnosis of hyperplasia and adenocarcinoma	

PS Disclosure; Page 19; 77pp; English.

XX Proteolins AM54349-WS4364 are examples of proteins produced in the

CC phase of the endometrium. The presence and quantity of these proteins

CC can be detected using 2D gel electrophoresis comprised of cell lysates.

CC The proteins can be used as biochemical markers to detect the phase of

CC the endometrium and can be measured in body fluids, obviating the need

CC for endometrial biopsies.

XX

XX Sequence 641 AA:

Query Match 100.0%; Score 3263; DB 19; Length 641;

Best Local Similarity 100.0%; Pred. No. 1,4e-224;

Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAAAAIGIDGFTYSCGVFQHGKVELIANDQGNFTTSTVAFTDTEELIGDAKNQYA 60

DB 1 MAAAAIGIDGFTYSCGVFQHGKVELIANDQGNFTTSTVAFTDTEELIGDAKNQYA 60

OY 61 LNPONTVDKAKRLIGRFEDPVVDSMKHMPVOYINDCDKPVYOVSKGTRKAFPEEIS 120

DB 61 LNPONTVDKAKRLIGRFEDPVVDSMKHMPVOYINDCDKPVYOVSKGTRKAFPEEIS 120

OY 121 SWVLTAKKEIAENYLGPTVNAVITVPAFVNDQSRQATKDAVYAGIAGVLTINEPTAA 180

DB 121 SWVLTAKKEIAENYLGPTVNAVITVPAFVNDQSRQATKDAVYAGIAGVLTINEPTAA 180

OY 181 IYAGLDRGTGGERNNYLFPLGGGTPEVSLITTDGIFFEVKAAGDTHLOGEDEDNRVLNH 240

DB 181 IYAGLDRGTGGERNNYLFPLGGGTPEVSLITTDGIFFEVKAAGDTHLOGEDEDNRVLNH 240

OY 241 FVEEFKRRKKKDISONKRAVVRRLTACEPAKRLTSSSTQASLELDSLFGIDFTYSTTRA 300

DB 241 FVEEFKRRKKKDISONKRAVVRRLTACEPAKRLTSSSTQASLELDSLFGIDFTYSTTRA 300

OY 301 REEELCSDLFEFSTLEPVEKALRQAKLIDQIHDIYVAGSTTRIPVOKLIDDFEFGNDLN 360

DB 301 REEELCSDLFEFSTLEPVEKALRQAKLIDQIHDIYVAGSTTRIPVOKLIDDFEFGNDLN 360

OY 361 KETIPDEAVAYGAOVAALIMDKSEBNVDLLIDVAELSLGIFLAGOVMTALIKRNSIT 420

DB 361 KETIPDEAVAYGAOVAALIMDKSEBNVDLLIDVAELSLGIFLAGOVMTALIKRNSIT 420

OY 421 PTKQTQIIFTTYSNDPGVLIQVDEGRAMTKNNMLGSEFELSIPAPGPOIETFTDI 480

DB 421 PTKQTQIIFTTYSNDPGVLIQVDEGRAMTKNNMLGSEFELSIPAPGPOIETFTDI 480

OY 481 DAMELTANTMADQSCAKMTATNDQCLSKETIRBQVQAEKKAEDPOBQENBSAKN 540

DB 481 DAMELTANTMADQSCAKMTATNDQCLSKETIRBQVQAEKKAEDPOBQENBSAKN 540

OY 541 ALESYAFNNKSAVEDBGLGKLSBDDKRYKLVRCQEVLSMLDANLLEDFEFHRRKYLE 600

DB 541 ALESYAFNNKSAVEDBGLGKLSBDDKRYKLVRCQEVLSMLDANLLEDFEFHRRKYLE 600

OY 601 QVCPNPIISGLYQACGRCGCGAGCGAGCGGCGSCPTETND 641

DB 601 QVCPNPIISGLYQACGRCGCGAGCGAGCGGCGSCPTETND 641

RESULT 2

AA023652 standard; protein: 641 AA.

AA023652:

05-JAN-2001 (first entry)

Human heat shock protein Hsp70.1 protein sequence S60 ID NO:4.

ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte CTL; immune response; infectious disease; malaria; cytotoxic T cell.

KM cytosolic; immunostimulant; cellular immune response inducer;

XX protozoacide; Leukemia; cancer.

XX Homo sapiens.

XX W0200049041-A1.

XX 24-AUG-2000.

PD 18-FEB-2000; 2000MO-JF00941.

XX 19-FEB-1999; 99JP-0041535.

XX (SUDE) SWITZROM ELECTRIC IND CO.

FA Shubara N, Udono H, Yui K;

PI WPI: 2000-543748/49.

DR

XX Fused protein capable of inducing cellular immune response, useful as

PT antigenic ingredient for drug compositions in preventing and/or treating

XX infectious diseases such as malaria or cancer

XX

PS Claim 3: Page 46-48; 72pp; Japanese.

XX The present invention describes a fused protein (1) prepared from a

CC heat shock protein and a protein containing the Atpase domain of a heat

CC shock protein. Also described are: (1) a drug composition containing (1)

CC as active ingredient; (2) a DNA encoding (1); (3) an expression vector

CC containing the DNA of (2); and (4) a transformant which can retain the

CC expression vector of (3). (1) has cytosolic, immunostimulant and

CC protozoacide activities, and can be used as a cellular immune response

CC inducer. (2) can be used as a vaccine against infectious diseases such as

CC malaria or cancer e.g., to provide systemic immunity against leukaemia.

CC The present sequence represents a specifically claimed heat shock

XX protein for use in a fused protein of the present invention.

XX

XX Sequence 641 AA:

Query Match 100.0%; Score 3263; DB 21; Length 641;

Best Local Similarity 100.0%; Pred. No. 1,4e-224;

Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAAAAIGIDGFTYSCGVFQHGKVELIANDQGNFTTSTVAFTDTEELIGDAKNQYA 60

DB 1 MAAAAIGIDGFTYSCGVFQHGKVELIANDQGNFTTSTVAFTDTEELIGDAKNQYA 60

OY 61 LNPONTVDKAKRLIGRFEDPVVDSMKHMPVOYINDCDKPVYOVSKGTRKAFPEEIS 120

DB 61 LNPONTVDKAKRLIGRFEDPVVDSMKHMPVOYINDCDKPVYOVSKGTRKAFPEEIS 120

OY 121 SWVLTAKKEIAENYLGPTVNAVITVPAFVNDQSRQATKDAVYAGIAGVLTINEPTAA 180

DB 121 SWVLTAKKEIAENYLGPTVNAVITVPAFVNDQSRQATKDAVYAGIAGVLTINEPTAA 180

OY 181 IYAGLDRGTGGERNNYLFPLGGGTPEVSLITTDGIFFEVKAAGDTHLOGEDEDNRVLNH 240

DB 181 IYAGLDRGTGGERNNYLFPLGGGTPEVSLITTDGIFFEVKAAGDTHLOGEDEDNRVLNH 240

OY 241 FVEEFKRRKKKDISONKRAVVRRLTACEPAKRLTSSSTQASLELDSLFGIDFTYSTTRA 300

DB 241 FVEEFKRRKKKDISONKRAVVRRLTACEPAKRLTSSSTQASLELDSLFGIDFTYSTTRA 300

OY 301 REEELCSDLFEFSTLEPVEKALRQAKLIDQIHDIYVAGSTTRIPVOKLIDDFEFGNDLN 360

DB 301 REEELCSDLFEFSTLEPVEKALRQAKLIDQIHDIYVAGSTTRIPVOKLIDDFEFGNDLN 360

OY 361 KETIPDEAVAYGAOVAALIMDKSEBNVDLLIDVAELSLGIFLAGOVMTALIKRNSIT 420

DB 361 KETIPDEAVAYGAOVAALIMDKSEBNVDLLIDVAELSLGIFLAGOVMTALIKRNSIT 420

QY	241	FVLRKARKRKHNDISQKKAAARELRTFCCEAKARTLSSTQASDLSLEIDFETYSITRA	300
OY	241	FVLRKARKRKHNDISQKKAAARELRTFCCEAKARTLSSTQASDLSLEIDFETYSITRA	300
DY	241	FVEERFKRRKHNDISQKKAAARELRTFCCEAKARTLSSTQASDLSLEIDFETYSITRA	300
QY	301	FEELCSDLSPFTSSLPYRKALMDAKLDKAOKHDAIVYSGSRPRPKOVLADDPNCRNTA	360
DY	301	FEELCSDLSPFTSSLPYRKALMDAKLDKAOKHDAIVYSGSRPRPKOVLADDPNCRNTA	360
DY	301	FEELCSDLSPFTSSLPYRKALMDAKLDKAOKHDAIVYSGSRPRPKOVLADDPNCRNTA	360
QY	361	KSIINDENAVAGAAVOALLIMDKDSERNVDLLILDVAPLSLGLETACGWFALIKRNSTT	420
DY	361	KSIINDENAVAGAAVOALLIMDKDSERNVDLLILDVAPLSLGLETACGWFALIKRNSTT	420
OY	481	PTRKQQLPFTTSINOPGVLYOVYGGSEKAMTKNNMLGRPEPLSGLPPAPRCVPQIENVTFDI	480
DY	481	PTRKQQLPFTTSINOPGVLYOVYGGSEKAMTKNNMLGRPEPLSGLPPAPRCVPQIENVTFDI	480
DY	541	ALSTVAEPFMKSAVEDDGJGKATKSTPAQCKKVYLDCQEVISMIDANTAEKDEFEHRKEELE	600
QY	601	QVCNPITISGLYOGAGGPFGGGFAQGSPKGSGGSPFTIEEVD	641
DY	601	QVCNPITISGLYOGAGGPFGGGFAQGSPKGSGGSPFTIEEVD	641
Db	601	QVCNPITISGLYOGAGGPFGGGFAQGSPKGSGGSPFTIEEVD	641
RESULT 5			
AAAB23653			
ID	AAAB23653 standard; protein: 640 AA.		
AC	AAAB23653;		
XX	05-JAN-2001 (first entry)		
XX	Human heat shock protein Hsp70 protein sequence SEQ ID NO:5.		
XX	ATPase; Hsp70; heat shock protein; cytoprotic T lymphocyte; CTL; Immune response; Infectious disease; malaria; cytotoxic T cell; cytoskeletal; immunostimulant; cellular immune response inducer; protooncogene; leukemia; cancer.		
OS	Homo sapiens.		
PN	WC0200049041-A1.		
PD	24-AUG-2000.		
PF	18-FEB-2000; 2000MOC-JP00941.		
PI	19-FEB-1999; 99JP-004135.		
PA	(SDME) SUMITOMO ELECTRIC IND CO.		
PI	Shinbara N, Udoho H, Yui K;		
DR	WPI: 2000-543748/49.		
CC	The present invention describes a fused protein (1) prepared from a polypeptide having an antigenic domain which can be used as a protective T-cell adjuvant and a protein containing the ATPase domain of a heat shock protein. Also described are: (1) a drug composition containing (1) as active ingredient; (2) a DNA encoding (1); (3) an expression vector containing the DNA of (2); and (4) a transformant which can retain the expression vector of (3). (1) has cytoskeletal, immunostimulant and		
CC	Claim 3: Page 49-52; 72pp; Japanese.		

CC protozoacide activities, and can be used as a cellular immune response inducer. The protein is useful as an active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer e.g. to provide systemic immunity against leukaemia. The present sequence represents a specifically claimed heat shock protein for use in a fused protein of the present invention.

Sequence 640 AA:

Query Match 99.4%; Score 3242.5; DB 21; Length 640;

Best Local Similarity 99.5%; Pred. No. 4e-223; Matches 638; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

1 MAAAAGIDLGTTTSCVGFQHGKVEIIANDGSKRTTSSVAFDTFRILGIDAAKNQYA 60
 1 MAAAAGIDLGTTTSCVGFQHGKVEIIANDGSKRTTSSVAFDTFRILGIDAAKNQYA 60
 61 LNPQTVFAKRLGKRGKDPVVSQDKMPFVINGCKRPVQSVYSGETAFAYPEIS 120
 61 LNPQTVFAKRLGKRGKDPVVSQDKMPFVINGCKRPVQSVYSGETAFAYPEIS 120
 121 SMVTRKKKEIAEAVLGYPVNAITVPAVFNDSQKATKDAGVAGLWVLRINEPTAA 180
 121 SMVTRKKKEIAEAVLGYPVNAITVPAVFNDSQKATKDAGVAGLWVLRINEPTAA 180
 181 IAVGLDRTGKGRNVLFDLGSGTFDVSLITDDGIFEYKATAGDTHLGGEDFNNRLVNH 240
 181 IAVGLDRTGKGRNVLFDLGSGTFDVSLITDDGIFEYKATAGDTHLGGEDFNNRLVNH 240
 241 FVEEERKRNKNDISQKNKAVRRLPTACEAKRTLSSTQASLEIDSLPEGIDFTTSTRA 300
 241 FVEEERKRNKNDISQKNKAVRRLPTACEAKRTLSSTQASLEIDSLPEGIDFTTSTRA 300
 301 RFEELCSULFRSTLEPEYKALDKAKIHOVLVVGSTRIIPKVKLLDGFNCGDLN 360
 301 RFEELCSULFRSTLEPEYKALDKAKIHOVLVVGSTRIIPKVKLLDGFNCGDLN 360
 361 KSIINDEAVAGAAVOAIIIMGDKSENVODLLILVAPSLGIEPTAGVWFLIKRNSTI 420
 361 KSIINDEAVAGAAVOAIIIMGDKSENVODLLILVAPSLGIEPTAGVWFLIKRNSTI 420
 421 PTGKOIIFTTYSNDQPGVLLQVYEGEERAMTKDNLLRRELISGIPPARQVQIETPPI 480
 421 PTGKOIIFTTYSNDQPGVLLQVYEGEERAMTKDNLLRRELISGIPPARQVQIETPPI 480
 481 DANGILAVNTADKSTCKANKITITNDGKLSKEETERNVOAEKRYAAEDVQERRSAA 540
 481 DANGILAVNTADKSTCKANKITITNDGKLSKEETERNVOAEKRYAAEDVQERRSAA 540
 540 ALSEYAFNKSASVEDGKIKISEADKKVLDLDCQEVYISMDANTLAEKDEFEHRKELE 600
 540 ALSEYAFNKSASVEDGKIKISEADKKVLDLDCQEVYISMDANTLAEKDEFEHRKELE 600
 600 QVNCPIISGLVQAGGPGEGAGQKGGSGSGPTIEVD 640

RESULT 5

AAAI0065 standard; Protein: 640 AA.

AAAI0065;

24-OCT-1997 (first entry)

Human heat shock protein 70.

Human: heat shock protein 70; HSP70; primer: probe; detection;

LC: intracellular; abnormal transcription; acute; chronic; sustained;

stress.

Homo sapiens.

XX JF08322577-A.
 XX 10-DEC-1996.
 XX 01-JUN-1995; 95UP-0158581.
 XX 01-JUN-1995; 95UP-0158581.
 XX (HOKI-) HOKEN KAGAKU KENKYUSHO KK.
 XX NPI: 1997-081088/08.
 XX N-PSDB: AAT58086.
 XX Description of abnormal transcription of HSP70 mRNA - using HSP70
 XX specific primer or probe "used in detection of human acute and
 XX chronic sustained stress load
 XX Claim 1: Fig 1; 13pp; Japanese.

The cDNA encoding the present sequence, human heat shock protein 70 (HSP70), is located on human chromosome HSP70 cDNA coding of (183-21) protein and is used to detect the abnormal transcription of intracellular HSP70 mRNA in human acute and chronic sustained stress load.

Sequence 640 AA:

Query Match 99.0%; Score 3239.5; DB 18; Length 640;

Best Local Similarity 99.2%; Pred. No. 3.4e-222; Matches 636; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

1 MAAAAGIDLGTTTSCVGFQHGKVEIIANDGSKRTTSSVAFDTFRILGIDAAKNQYA 60
 1 MAAAAGIDLGTTTSCVGFQHGKVEIIANDGSKRTTSSVAFDTFRILGIDAAKNQYA 60
 61 LNPQTVFAKRLGKRGKDPVVSQDKMPFVINGCKRPVQSVYSGETAFAYPEIS 120
 61 LNPQTVFAKRLGKRGKDPVVSQDKMPFVINGCKRPVQSVYSGETAFAYPEIS 120
 121 SMVTRKKKEIAEAVLGYPVNAITVPAVFNDSQKATKDAGVAGLWVLRINEPTAA 180
 121 SMVTRKKKEIAEAVLGYPVNAITVPAVFNDSQKATKDAGVAGLWVLRINEPTAA 180
 181 IAVGLDRTGKGRNVLFDLGSGTFDVSLITDDGIFEYKATAGDTHLGGEDFNNRLVNH 240
 181 IAVGLDRTGKGRNVLFDLGSGTFDVSLITDDGIFEYKATAGDTHLGGEDFNNRLVNH 240
 241 FVEEERKRNKNDISQKNKAVRRLPTACEAKRTLSSTQASLEIDSLPEGIDFTTSTRA 300
 241 FVEEERKRNKNDISQKNKAVRRLPTACEAKRTLSSTQASLEIDSLPEGIDFTTSTRA 300
 301 RFEELCSULFRSTLEPEYKALDKAKIHOVLVVGSTRIIPKVKLLDGFNCGDLN 360
 301 RFEELCSULFRSTLEPEYKALDKAKIHOVLVVGSTRIIPKVKLLDGFNCGDLN 360
 361 KSIINDEAVAGAAVOAIIIMGDKSENVODLLILVAPSLGIEPTAGVWFLIKRNSTI 420
 361 KSIINDEAVAGAAVOAIIIMGDKSENVODLLILVAPSLGIEPTAGVWFLIKRNSTI 420
 421 PTGKOIIFTTYSNDQPGVLLQVYEGEERAMTKDNLLRRELISGIPPARQVQIETPPI 480
 421 PTGKOIIFTTYSNDQPGVLLQVYEGEERAMTKDNLLRRELISGIPPARQVQIETPPI 480
 481 DANGILAVNTADKSTCKANKITITNDGKLSKEETERNVOAEKRYAAEDVQERRSAA 540
 481 DANGILAVNTADKSTCKANKITITNDGKLSKEETERNVOAEKRYAAEDVQERRSAA 540
 540 ALSEYAFNKSASVEDGKIKISEADKKVLDLDCQEVYISMDANTLAEKDEFEHRKELE 600
 540 ALSEYAFNKSASVEDGKIKISEADKKVLDLDCQEVYISMDANTLAEKDEFEHRKELE 600

[illegible][illegible]

QY 601 QWNCNIIISGLYQAGG-PG--PGGF--GAGCPKGGSGSGPTIEVD 641
 DB 601 KVCNIIITRLYQSGAGMGPGMGPGGAGAPPGGAGSSGPTIEVD 646

RESULT 14
 AAB3649
 ID AAB3649 standard; protein: 646 AA.

AAB3649;

05-JAN-2001 (first entry)

Mouse heat shock protein Hsc70 protein sequence SPO ID NO:1.

ATPase; Hsp70; heat shock protein; cytoxic T lymphocyte; CTL;
 immune response; infectious disease; malaria; cytoxic T cell;
 cytoxic; immunostimulant; cellular immune response inducer;
 protozoicidal; leukemia; cancer.

Mus sp.

MO200049041-A1.

24-AUG-2000.

18-FEB-2000; 2000MO-JP00941.

19-FEB-1999; 99JP-0041535.

(SIME) SUMITOMO ELECTRIC IND CO.

Shinbara N, Udono H, Yui K;

WPI: 2000-543748/49.

Fused protein capable of inducing cellular immune response, useful as
 active ingredient for drug compositions in preventing and/or treating
 infectious diseases such as malaria or cancer

Claim 3; Page 36-39; 72pp; Japanese.

The present invention describes a fused protein (1) prepared from a
 peptide containing a CTL (cytotoxic T lymphocyte) antigen, and a heat
 shock protein. Also described are: (1) a drug composition containing (1)
 as active ingredient; (2) a DNA encoding (1); (3) an expression vector
 containing the DNA of (2); (4) a transformant which can retain the
 expression vector of (3); (1) has cytoskeletal, immunostimulant and
 protozoicidal activities, and can be used as a cellular immune response
 inducer, immunostimulant, immunostimulant, immunostimulant, and
 immunostimulant in preventing and/or treating infectious diseases such as
 malaria or cancer e.g. to provide systemic immunity against leukemia.
 The present sequence represents a specifically claimed heat shock
 protein for use in a fused protein of the present invention.

Sequence 646 AA:

Query Match 87.7%; Score 2862.5; DB 21; Length 646;
 Best Local Similarity 85.8%; Pred No. 5.7e-196;
 Matches 554; Conservative 47; Mismatches 40; Indels 5; Gaps 3;

QY 1 MAAAAGAGIDGTTTSCVGFQHKKEIINDDGKRTTSYVAFDTERLIGDAAKNVYA 60
 DB 1 MSNGAVGIDGTTTSCVGFQHKKEIINDDGKRTTSYVAFDTERLIGDAAKNVYA 60
 QY 6 LINDQVFAKRLIGKSPVQVQSGMHPVQVINGKSKKQVSKYKATAPYEZIS 120
 DB 6 LINDQVFAKRLIGKSPVQVQSGMHPVQVINGKSKKQVSKYKATAPYEZIS 120
 QY 121 SWITFKKEIAEAVLGKTYNNAVTVPAVFNDSORATKDGVTGAGLNLRLINEFTAA 180
 DB 121 SWITFKKEIAEAVLGKTYNNAVTVPAVFNDSORATKDGVTGAGLNLRLINEFTAA 180

DB 121 SWITFKKEIAEAVLGKTYNNAVTVPAVFNDSORATKDGVTGAGLNLRLINEFTAA 180
 QY 181 IAVGIDPTGKERNVLIFDGSGTDFVSIITDGTFEVKNATAGTHLGSEDPNKLNVN 240
 DB 181 IAVGIDPTGKERNVLIFDGSGTDFVSIITDGTFEVKNATAGTHLGSEDPNKLNVN 240
 QY 241 FVEEFKRRKKRDLSQKRAVRLKTCRRKRLPTSSSTOASLRLSEIDFTSTIRP 300
 DB 241 FVEEFKRRKKRDLSQKRAVRLKTCRRKRLPTSSSTOASLRLSEIDFTSTIRP 300
 QY 301 REPELSDLPFSTLEPVERALDKRLDKAOLHDLVGGSTRIPVKNLLDFFNGRLN 360
 DB 301 REPELSDLPFSTLEPVERALDKRLDKAOLHDLVGGSTRIPVKNLLDFFNGRLN 360
 QY 361 KSLINDEAVAGAAVOAALIMDGSNNVODLLDVPAPSLGIEPAGCWVRLAKKNSSTI 420
 DB 361 KSLINDEAVAGAAVOAALIMDGSNNVODLLDVPAPSLGIEPAGCWVRLAKKNSSTI 420
 QY 421 PKTQOLPFTTYSNPGVLTQVYEGSRAMTKNNMLDRELSGIPAPKQVQIEVFDI 480
 DB 421 PKTQOLPFTTYSNPGVLTQVYEGSRAMTKNNMLDRELSGIPAPKQVQIEVFDI 480
 QY 481 DANGILVATDTSKSGKANKITITNKRSLKSELEHMYOAKRKADBPQREPVSKN 540
 DB 481 DANGILVATDTSKSGKANKITITNKRSLKSELEHMYOAKRKADBPQREPVSKN 540
 QY 541 ALESTAFNKSANVEDGKGRKISBAUKKKVYLDKCEVYSMLDANLALBKDEPHEKKELE 600
 DB 541 ALESTAFNKSANVEDGKGRKISBAUKKKVYLDKCEVYSMLDANLALBKDEPHEKKELE 600
 QY 601 QWNCNIIISGLYQAGG-PG--PGGF--GAGCPKGGSGSGPTIEVD 641
 DB 601 KVCNIIITRLYQSGAGMGPGMGPGGAGAPPGGAGSSGPTIEVD 646

RESULT 15
 AAB3649
 ID AAB3649 standard; protein: 646 AA.

AAB3649;

14-AUG-1998 (first entry)

Heat shock cognate 71 kd protein.

Endometrium; hyperplasia; adenocarcinoma; proliferative phase;
 2D gel electrophoresis; detection.

Osaka University.

MO9610291-A1.

12-MAR-1998.

05-SEP-1997; 97MO-GB02394.

08-APR-1997; 97GB-0007132.

06-SEP-1996; 96GB-0018500.

(CLIN-) CENT CLINICAL & BASIC RES.

Byrjalsen I, Fey SJ, Larsen P;

WPI: 1998-207057/18.

Biochemical markers of human endometrium - useful for, e.g.
 diagnosis of hyperplasia and adenocarcinoma
 Disclosure: Page 23; 77pp; English.
 Proteins AAB5349-W5364 are examples of proteins produced in the
 endometrium during the hyperplasia, adenocarcinoma or proliferative
 phase of the endometrium. The presence and quantities of these proteins

CC can be detected using 2D gel electrophoresis comparison of cell lysates.
 CC The proteins can be used as biochemical markers to detect the phase of
 CC the endometrium and can be measured in body fluids, obviating the need
 CC for endometrial biopsies.
 XX

Sequence 646 AA:

Query Match 87.6%; Score 2859.5; DB 19; Length 646;
 Best Local Similarity 85.6%; Pred. No. 9.3e-196;
 Matches 553; Conservative 48; Mismatches 40; Indels 5; Gaps 3;

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QY 1 MAAKAAIGDGGTYSCNGVGVKVTIANDGNCNTPSYVFTDPRFELIGDAKNQVA 60
DB 1 MKNQPAVGIDGGTYSCVGVFQHGKVELIANDGNCNTPSYVFTDPRFELIGDAKNQVA 60
QY 61 LNPQNTVDAKRLIGKFGDPVYOSDKMHPFOVINDGDKPKVOYSKGTAKAPYEELS 120
DB 61 MNPNTVDAKRLIGKFGDPVYOSDKMHPVNDGDKPKVOYSKGTAKAPYEELS 120
QY 121 SWVLTEKKEITAEYLYGPTNAVTATVPAYPNDSROATKQACVYAGIANTLTINPTAA 180
DB 121 SWVLTEKKEITAEYLYGRTYNAVYVTPAYPNDSROATKQAGTIAGIANTLTINPTAA 180
QY 181 IAYGLDRGKGERNYLLFDLGGSTFDVSLITLDGIFEVAKATAGDTHLGGEDFNRLVNH 240
DB 181 IAYGLDRKVAERNYLLFDLGGSTFDVSLITLEDGIFEVAKTAGDTHLGGEDFNRLVNH 240
QY 241 PVCEFRKHKKDISSNKRAYRRLFTACERAKETLSSQASLFDLSLFGIDFYSITRA 300
DB 241 FLAEFRKHKKDISSNKRAYRRLFTACERAKETLSSQASLEIDSLYEGIDFYSITRA 300
QY 301 REBELSDLFESTLEPVEKALRDQAKIDHDLYVCGSTRIPKVLQDFPFGKDLN 360
DB 301 REBELADLFEGILDPEKALRDQAKIDSDHDLYVCGSTRIPKVLQDFPFGKDLN 360
QY 361 KSIINPEAVNAGAAVOAALIMCKSPNODLLDVAPLSLGIETAGGYMTALIKRSTI 420
DB 361 KSIINPEAVNAGAAVOAALIMCKSPNODLLDVAPLSLGIETAGGYMTALIKRNTI 420
QY 421 PTKOTIPTTYSNDQPGVLTQYVEGRAMKDNMLGREFELSGIPAPRGVPOIEVTFDI 480
DB 421 PTKOTIPTTYSNDQPGVLTQYVEGRAMKDNMLGREFELSGIPAPRGVPOIEVTFDI 480
QY 481 DANGILANTATSKGAKTITTDNKGRLSKERTPRMVOGEAKYKADDEQGEREVSAN 540
DB 481 DANGILNWSAVDSKGEKKTITTDNKGRLSKREDIERMVOGEAKYKADDEQKORDEVSAN 540
QY 541 ALSEYAFNNKSAVEDDELKGIKISEADKKVLDKCEVITSWLDANTLAERKDFEKKRKELE 600
DB 541 SLESTAFNNKATYEDERLKDNDKOKLIDKCNELINMLDKNQTKAEKEFEHQKLELE 600
QY 601 QVCMPLIISGLYQAG-PC--PGGF--CAQPGKSGSGSPTEYD 641
DB 601 KVCNPIITKLYQAGPCGPGGPGGAPGSGASSPTEYD 646

```

Search completed: December 4, 2002, 16:41:55
 Job time : 41 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2002, 16:50:13 : Search time 38 seconds
(without alignments)
3475.689 Million cell updates/sec

Title: US-09-646-835-1

Sequence: 1 MAAKAAAGIDLTFTYSCGV.....FGAGPKGSSSGPTIEVD 641

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Lasting first 45 summaries

Database :
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mammal:*
8: sp.invertebrate:*
9: sp.plant:*
10: sp.plant:*
11: sp.invertebrate:*
12: sp.virus:*
13: sp.invertebrate:*
14: sp.invertebrate:*
15: sp.bacteria:*
16: sp.bacteria:*
17: sp.archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	318	49.6	640	6	08WNS9 canis falli
2	150	23.4	151	4	09QDC1 09qgcl homo sapien
3	110	11.1	111	11	08WNS9 canis falli
4	101	15.8	642	11	08WNS9 canis falli
5	101	15.8	642	11	08WNS9 canis falli
6	73	11.4	455	11	063718 ratu mus
7	72	11.2	641	4	075634 075634 homo sapien
8	72	11.2	641	4	0960C9 0960C9 homo sapien
9	60	9.4	228	11	061698 061698 mus musculu
10	58	9.0	639	13	08WNS9 canis falli
11	58	9.0	639	13	08WNS9 canis falli
12	58	9.0	639	13	08WNS9 canis falli
13	55	8.6	637	13	08WNS9 canis falli
14	55	8.6	637	13	08WNS9 canis falli
15	55	8.6	637	13	08WNS9 canis falli
16	55	8.6	637	13	08WNS9 canis falli

17	55	8.6	641	11	088686 088686 mus musculu
18	55	8.6	644	5	09SV47 09SV47 artemia san
19	55	8.6	658	13	091NC1 091NC1 brachydanio
20	54	8.4	638	13	08WNS9 08WNS9 xiphophorus
21	54	8.4	640	13	08WNS9 08WNS9 xiphophorus
22	53	8.3	493	4	091386 091386 homo sapien
23	53	8.3	493	4	091386 091386 homo sapien
24	53	8.3	566	6	095189 095189 mecca fasc
25	53	8.3	646	13	073885 073885 gallus gall
26	53	8.3	647	13	091993 091993 xenopus lae
27	53	8.3	651	5	08SX04 08SX04 drosophila
28	53	8.3	651	19	080V14 080V14 amygdala m
29	52	8.1	643	13	079984 079984 brachydanio
30	52	8.1	643	13	079984 079984 brachydanio
31	51	8.0	779	6	095J00 095J00 equus cabal
32	49	7.6	247	13	098901 098901 equus cabal
33	49	7.6	367	13	098899 098899 fugu rubrip
34	49	7.6	646	5	001948 001948 trichella
35	48	7.5	552	11	09QW01 09QW01 mus musculu
36	48	7.5	645	10	0959N1 0959N1 mus musculu
37	47	7.3	650	5	09N102 09N102 segalins oe
38	47	7.3	650	5	09N102 09N102 segalins oe
39	45	7.0	599	5	08WNS9 08WNS9 crassostrea
40	45	7.0	636	5	018474 018474 biophalari
41	45	7.0	636	5	043433 043433 biophalari
42	45	7.0	639	13	098900 098900 fugu rubrip
43	45	7.0	646	5	094614 094614 mesocetoid
44	45	7.0	659	5	09XJ72 09XJ72 echinosce
45	45	7.0	653	5	024789 024789 echinosce

ALIGNMENTS

RESULT 1

08WNS9 PRELIMINARY: PRT: 640 AA.

01-MAR-2002 (TREMBLrel. 20. Created)

01-MAR-2002 (TREMBLrel. 20. Last sequence update)

01-JUN-2002 (TREMBLrel. 21. Last annotation update)

Heat shock protein 70.

Heat shock protein 70.

Heat shock protein 70.

Heat shock protein 70.

Heat shock protein 70.

Heat shock protein 70.

Heat shock protein 70.

Heat shock protein 70.

Heat shock protein 70.

Heat shock protein 70.

Heat shock protein 70.

Heat shock protein 70.

Heat shock protein 70.

Heat shock protein 70.

Heat shock protein 70.

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Oy 216 IFEVAKATGOTHLGSEDFNRLVNHVEERKKRKKDLSQNKBAVRLPRLACRAKRTIS 275
Db 216 IFEVAKATGOTHLGSEDFNRLVNHVEERKKRKKDLSQNKBAVRLPRLACRAKRTIS 275
Oy 276 SSTQASLEIDSLPEGIDPYSITPRAFEELGSDLEFSTLEPYVAKALNDKALDAAQIHLY 335
Db 276 SSTQASLEIDSLPEGIDPYSITPRAFEELGSDLEFSTLEPYVAKALNDKALDAAQIHLY 335
Oy 336 LVGSGSTRIPKVKOLLDFPNSRLNKSINDEAVAVGAQVAALIMDKSENVDLLD 395
Db 336 LVGSGSTRIPKVKOLLDFPNSRLNKSINDEAVAVGAQVAALIMDKSENVDLLD 395
Oy 396 VAPSLGTEFTAGCVTAL 413
Db 396 VAPSLGTEFTAGCVTAL 413

RESULT 2
Oy 0900C1 PRELIMINARY: PRT: 151 AA.
AC 0900C1:
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
Db HSP70.1:
DR HSP70.1: HSP70.1, last annotation update.
DR HSP70.2: HSP70.2, last annotation update.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
NX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RA STRAIN=2194376; PubMed=10092532; Demura H.;
RA "An additional exon of stress-inducible heat shock protein 70 gene
RT (HSP70-1).";
RL Biochem. Biophys. Res. Commun. 237:193-198(1999).
CC -1 SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL: AB018045; BAAT735.1; -.
DR HSP70.1: HSP70.1, last annotation update.
DR HSP70.2: HSP70.2, last annotation update.
DR PRINTS: PR001012; HSP70.1.
DR PRODOM: PD000089; HEATSHOCK70.
DR PROSITE: PS00329; HSP70.2; 1.
KW ATP-binding; 151
FT NON-TER
SO SEQUENCE 151 AA; 16473 MW; 5C504568D92CC850 CRC64;

Query Match 23.4%; Score 150; DB 4; Length 151;
Best Local Similarity 100.0%; Pred. No. 2e-146;
Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
GN Hsp 70.
NC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NX NCBI_TaxID=10116;
[1]
RN SEQUENCE FROM N.A.
RA STRAIN=4190258; PubMed=8141767; Dillmann W.H.;
RA "Isolation of a novel inducible rat heat shock protein (HSP70) gene
RT and its expression during ischemia/hypoxia and heat shock.";
RL Biochem. J. 298:561-569(1994).
CC -1 SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR EMBL: X75357; CA53140.1; -.
DR HSP70.1: HSP70.1, last annotation update.
DR HSP70.2: HSP70.2, last annotation update.
DR PRINTS: PR001012; HSP70.1.
DR PRODOM: PD000089; HSP70.1.
DR PROSITE: PS00329; HSP70.1; 1.
DR PROSITE: PS01036; HSP70.3; 1.
KW ATP-binding; 641 AA; 69978 MW; AA123439AB2D03 CRC64;
SO SEQUENCE 641 AA; 70079 MW; F49C35602AEAE334 CRC64;

Query Match 17.8%; Score 114; DB 11; Length 641;
Best Local Similarity 100.0%; Pred. No. 1.4e-108;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 313 TLEPEKALRDALKKQIHDLVVGSGSTRIPKVKOLLDFPNSRLNKSINDEAVAVG 372
Db 313 TLEPEKALRDALKKQIHDLVVGSGSTRIPKVKOLLDFPNSRLNKSINDEAVAVG 372
Oy 373 AAVQALIMDKSENVDLLDVAFLGTEFTAGCVTALIKRNSPTPTROT 426
Db 373 AAVQALIMDKSENVDLLDVAFLGTEFTAGCVTALIKRNSPTPTROT 426

RESULT 4
Oy 0900C5 PRELIMINARY: PRT: 641 AA.
AC 0900C5:
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
Db HSP70.
DR HSP70.1: HSP70.1, last annotation update.
DR HSP70.2: HSP70.2, last annotation update.
DR HSP70.3: HSP70.3, last annotation update.
DR PRINTS: PR001012; HSP70.1.
DR PRODOM: PD000089; HEATSHOCK70.
DR PROSITE: PS00329; HSP70.1; 1.
DR PROSITE: PS00329; HSP70.2; 1.
DR PROSITE: PS01036; HSP70.3; 1.
KW ATP-binding; 641 AA; 70079 MW; F49C35602AEAE334 CRC64;
SO SEQUENCE 641 AA; 70079 MW; F49C35602AEAE334 CRC64;

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Query Match      15.8%: Score 101; DB 11; Length 641;
Best Local Similarity 100.0%: Pred. No. 3.9e-95;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 138 PYTNNAVITPAVFNSQKQATKDAAGVYAGLVATRIHEPFAAIAVGLDRTKGERNVLI 197
    |||||||
DB 138 PYTNNAVITPAVFNSQKQATKDAAGVYAGLVATRIHEPFAAIAVGLDRTKGERNVLI 197

OY 198 FDLSGGTFPVVSLITLDDIPEVKATAGDTHLGEDEPFNRLV 238
    |||||||
DB 198 FDLSGGTFPVVSLITLDDIPEVKATAGDTHLGEDEPFNRLV 238

RESULT 5
OY25V6 PRELIMINARY: PRT: 642 AA.
ID OY25V6:
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE HSP70_2002 (TREMBlrel. 20, Last annotation update)
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RA Rosen L., Madan A., Qin S., Hall J., Dahl T., James R., Diethoff R.,
RA Schaffer T., Kascliffe A., Abassi L., Loretz C., Lusky S., Hood L.;
RT Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.
CC 1- STIMULATORY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
EMBL: AF109506; AAC84188.1;
CC 2- HEAT SHOCK: HSP70_1;
DR Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DR Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
DR PROSITE: PS00297; HSP70_1; UNKNOWN.1.
DR PROSITE: PS00329; HSP70_3; UNKNOWN.1.
DR PROSITE: PS01036; HSP70_3; UNKNOWN.1.
KW ATP-binding.
SQ
SEQUENCE 642 AA: 70176 MW: 489908130C23D88 CRC64;
SO
Query Match      15.8%: Score 101; DB 11; Length 642;
Best Local Similarity 100.0%: Pred. No. 3.9e-95;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 138 PYTNNAVITPAVFNSQKQATKDAAGVYAGLVATRIHEPFAAIAVGLDRTKGERNVLI 197
    |||||||
DB 138 PYTNNAVITPAVFNSQKQATKDAAGVYAGLVATRIHEPFAAIAVGLDRTKGERNVLI 197

OY 198 FDLSGGTFPVVSLITLDDIPEVKATAGDTHLGEDEPFNRLV 238
    |||||||
DB 198 FDLSGGTFPVVSLITLDDIPEVKATAGDTHLGEDEPFNRLV 238

RESULT 6
OY3718 PRELIMINARY: PRT: 455 AA.
ID OY3718:
AC O63118:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Heat shock rotein 70 (fragment).
OS Rattus rattus (Black rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10117;
RN 11
RP SEQUENCE FROM N.A.
RA Angeletti B., Passarelli F., Orru D., Pascale E., Butler R.H.,
RA d'Ambrosio E.;

```

```

RT Cloning of cDNA for the rat inducible 70KD heat shock protein
RT (HSP70).";
RT Submitted (NOV-1993) to the EMBL/Genbank/DBJ databases.
CC 1- STIMULATORY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC 2- HEAT SHOCK: HSP70_1;
DR Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DR Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
DR PROSITE: PS00301; HEATSHOCK70.
DR PROSITE: PS00089; HSP70_1.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
KW ATP-binding.
SQ
SEQUENCE 455 AA: 50405 MW: 0P45F1CBA1E2971 CRC64;
SO
Query Match      11.4%: Score 73; DB 11; Length 455;
Best Local Similarity 100.0%: Pred. No. 2.6e-56;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 166 GIVWRIRINPEPMAAIAVGLDRTKGERNVITFDLSGGTFPVVSLITLDDIPEVKATAGD 225
    |||||||
DB 134 GIVWRIRINPEPMAAIAVGLDRTKGERNVITFDLSGGTFPVVSLITLDDIPEVKATAGD 193

OY 226 THLSGDEPFNRLV 238
    |||||||
DB 194 THLSGDEPFNRLV 206

RESULT 7
OY75634 PRELIMINARY: PRT: 641 AA.
ID OY75634:
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE Heat shock protein 70 testis variant.
OS HSPALL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RA MEDICINE-98351992; PubMed-9685725;
RA Ito Y., Ando H., Ando H., Saijoh Y., Inoko H., Fujimoto H.;
RT Genomic structure of the spermatid-specific HSP70 homolog gene
RT located in the class III region of the major histocompatibility
RT complex of mouse and man.
RT J. Biochem. 124:347-353(1998).
DB Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DB Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
DB PROSITE: PS01307; HSP70_1.
DR Interpro: IPR001023; HSP70.
DR Pfam: PF00012; HSP70_1.
DR PRINTS: PR00301; HEATSHOCK70.
DR PROSITE: PS00089; HSP70_1.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
SQ
SEQUENCE 641 AA: 70437 MW: 3033857D43019F7 CRC64;
SO
Query Match      11.2%: Score 72; DB 4; Length 641;
Best Local Similarity 100.0%: Pred. No. 3.9e-65;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 388 VOGLLLDVAPLSLGIEFAGVYALIKKNSSTLPKQKQIFPTYSNDQPCVLIQVDEGR 447
    |||||||
DB 390 VOGLLLDVAPLSLGIEFAGVYALIKKNSSTLPKQKQIFPTYSNDQPCVLIQVDEGR 449

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QY 448 AMTKONNLGRF 459
DB 450 AMTKONNLGRF 461

RESULT 8

0960C9 PRELIMINARY; PRT: 641 AA.

AC 0960C9 01-DEC-2001 (TREMblrel. 19, Created)

DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)

DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)

DE Heat shock protein.

OS HSP70-1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.

RA Hiraoka M., Yamaguchi H., Imai K., Shimada J.,

RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.

EN [2]

RP SEQUENCE FROM N.A.

RA Shima S., Taniya G., Oka A., Inoko H.,

RT Shima S., Taniya G., Oka A., Inoko H.,

CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

DR EMBL: AP000503; BAB3101.1;

DR InterPro: IPR01023; Hsp70.1.

DR Pfam: PF00012; Hsp70.1.

DR ProDom: PD000089; Hsp70.1.

DR PROSITE: PS00297; Hsp70.1; UNKNOWN.1.

DR PROSITE: PS00328; Hsp70.2; UNKNOWN.1.

DR PROSITE: PS1036; Hsp70.3; UNKNOWN.1.

DR ATP-binding.

KM SEQUENCE 641 AA; 70405 MW; 303385ED4300440 CRC64;

SO

Query Match 11.2%; Score 72; DB 4; Length 641;

Best Local Similarity 100.0%; Pred. No. 3.9e-65;

Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 368 VODLLILVAPSLCTGCGVMTALIKRSTTGCGITFTTSNQCGLIYVGRGR 447

DB 390 VODLLILVAPSLCTGCGVMTALIKRSTTGCGITFTTSNQCGLIYVGRGR 449

QY 448 AMTKONNLGRF 459

DB 450 AMTKONNLGRF 461

RESULT 9

061698 PRELIMINARY; PRT: 228 AA.

AC 061698 01-NOV-1996 (TREMblrel. 01, Created)

DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)

DE 01-MAR-2002 (TREMblrel. 21, Last annotation update)

DE Heat shock protein (Hsp68) (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.

RA Lowe D.G., Moran L.A.,

RT Molecular cloning and analysis of DNA complementary to three mouse

RL M-68,000 heat shock protein mRNAs.;

DE EMBL: M12573; AAAT763.1;

DR HSP70; E06109; ICR.

DR MCD: M01.99517; Hsp70-1.

DR InterPro: IPR01023; Hsp70.

DR Pfam: PF00012; Hsp70.1.

DR ProDom: PD000089; Hsp70.1.

DR NON_TER

SO SEQUENCE 228 AA; 24872 MW; BD7A09314CE0FEDC CRC64;

Query Match 9.4%; Score 60; DB 11; Length 228;

Best Local Similarity 100.0%; Pred. No. 3.9e-53;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 464 ITPAPGCVQIYVTFEDIDANGILNWTATDTSRGAKTITTDKRLSREIRFVAVQAE 523

DB 50 ITPAPGCVQIYVTFEDIDANGILNWTATDTSRGAKTITTDKRLSREIRFVAVQAE 109

RESULT 10

0988986 PRELIMINARY; PRT: 247 AA.

AC 0988986 01-FEB-1997 (TREMblrel. 02, Created)

DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)

DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)

DE 70 kDa heat-shock protein (Fragment).

OS Hsp70-1.

OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;

CC Tetraodontidae; Takifugu.

NCBI_TaxID=31033;

RP SEQUENCE FROM N.A.

RA MEDLINE-9928127; PubMed-10357235;

RT "Short-term alkali relationships, genomic organization and sequence

comparisons of a cluster of five Hsp70 genes in Fugu rubripes."

RL Cell Mol. Life Sci. 55:668-678(1999).

CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

DR EMBL: Y08576; CA69890.1;

DR HSP70; P08107; HMO.

DR InterPro: IPR01023; Hsp70.

DR ProDom: PD000089; Hsp70.1.

DR PROSITE: PS00297; Hsp70.1.

DR PROSITE: PS00328; Hsp70.2; 1.

DR ATP-binding.

KM SEQUENCE 247 247 26747 MW; IFS1A95B09411732 CRC64;

SO

Query Match 9.0%; Score 58; DB 13; Length 247;

Best Local Similarity 100.0%; Pred. No. 4.9e-51;

Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATGIDGFTTSCVCGFQHKVEIILNDOGKRTTSTVATFDTRILGDAAANOVALNP 63

DB 8 ATGIDGFTTSCVCGFQHKVEIILNDOGKRTTSTVATFDTRILGDAAANOVALNP 65

RESULT 11

073922 PRELIMINARY; PRT: 639 AA.

AC 073922 01-AUG-1998 (TREMblrel. 07, Created)

DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)

DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)

DE Heat shock protein 70.

OS Oryzochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

CC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidae;

Best Local Similarity 100.0%; Pred. No. 3e-48;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AIGIDIGTTTSCYGVFOHKEVIANDGKRTPTSVAFDTETRLIGDAARNOVA 60
|||||
DB 8 AIGIDIGTTTSCYGVFOHKEVIANDGKRTPTSVAFDTETRLIGDAARNOVA 62

RESULT 15

Q99KND7 PRELIMINARY; PRT; 633 AA.

AC Q99KND7

DT 01-JUN-2001 (TRENBLREL. 17, Created)

DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)

DT 01-MAR-2002 (TRENBLREL. 20, Last annotation update)

DE Heat shock protein, 70 kDa 2.

DS HSP70-2.

OS Mus musculus (Mouse).

OC Cell adhesion; Hemopoiesis; Hemostasis; Granulata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TextID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Strausberg R.; Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

CC 1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

DR PROSITE: PS00112; HSP70/14.1; ..

DR HSP; P19120; HSC

DR MCD; MGI:96243; HSP70-2.

DR InterPro: IPR001023; Hsp70.

DR Pfam: PF00012; HSP70; 1.

DR PRINTS: PR00301; HEATSHOCK70.

DR PRODOM: PD00089; HSP70; 1.

DR PROSITE: PS00326; HSP70; 1.

DR PROSITE: PS01036; HSP70_3; 1.

KW ATP-binding.

SQ SEQUENCE 633 AA: 69641 MW: 695773c7effa69f cr64;

Query Match

Best Local Similarity 8.6%; Score 55; DB 11; Length 633;

Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AIGIDIGTTTSCYGVFOHKEVIANDGKRTPTSVAFDTETRLIGDAARNOVA 60
|||||
DB 7 AIGIDIGTTTSCYGVFOHKEVIANDGKRTPTSVAFDTETRLIGDAARNOVA 61

Search completed: December 4, 2002, 16:52:44
Job time : 40 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2002, 16:50:56 : Search time 16 seconds
(Without alignments)
1178,756 Million cell updates/sec

Title: US-09-646-835-1

Sequence: 641
1 NAKAAAGIDLD7TYSCGV.....FGAGPKSSSGPTTEVD 641

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents, AA:*

1: /cgn2.6/pdataa1/1aa/5A.COMB.pep:*

2: /cgn2.6/pdataa1/1aa/5B.COMB.pep:*

3: /cgn2.6/pdataa1/1aa/6A.COMB.pep:*

4: /cgn2.6/pdataa1/1aa/6B.COMB.pep:*

5: /cgn2.6/pdataa1/1aa/6C.COMB.pep:*

6: /cgn2.6/pdataa1/1aa/6aack11est1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	8.3	646	1	US-08-441-139-14
2	53	8.3	890	4	US-09-513-783A-174
3	47	7.3	643	4	US-08-797-358B-3
4	48	4.4	339	4	US-08-928-692-52
5	28	4.4	339	4	US-09-319-972-52
6	20	3.6	515	1	US-08-214-383-2
7	19	3.0	649	4	US-09-066-047-5
8	19	3.0	649	4	US-09-066-047-5
9	18	2.8	18	1	US-08-240-514-37
10	18	2.8	18	2	US-08-612-302A-37
11	18	2.8	616	4	US-09-114-001C-3646
12	18	2.8	655	4	US-09-632-538C-36
13	17	2.7	17	2	US-08-480-190-132
14	17	2.7	17	2	US-08-480-190-132
15	17	2.7	17	2	US-08-441-139-16
16	17	2.5	42	6	US-08-441-139-16
17	15	2.5	516523-15	7545-132	Sequence 133, App
18	17	2.5	80	1	US-08-464-164-4
19	16	2.5	80	1	US-08-338-057-4
20	16	2.5	80	2	US-08-668-416-4
21	16	2.5	187	6	5196523-13-139-11
22	16	2.5	624	1	US-08-441-139-11
23	16	2.5	666	1	US-08-441-139-16
24	16	2.5	682	1	US-08-441-139-2
25	15	2.3	15	2	US-08-480-190-133
26	15	2.3	15	2	US-08-488-379-133
27	15	2.3	15	5	PCT-US93-07545-133

28	15	2.3	79	6	5196523-11	Patent No. 5196523
29	15	2.3	168	1	US-08-441-139-10	Sequence 10, App
30	15	2.3	183	4	US-09-556-877-301	Sequence 301, App
31	15	2.3	183	4	US-09-620-412C-301	Sequence 301, App
32	15	2.3	641	1	US-08-441-139-4	Sequence 4, App1
33	15	2.3	679	1	US-08-441-139-5	Sequence 5, App1
34	15	2.3	5196523-15	7545-132	Sequence 133, App	Sequence 133, App
35	13	2.0	607	2	US-08-472-534-5	Sequence 2, App
36	12	1.9	77	6	5196523-7	Sequence 7, App
37	11	1.7	11	6	5196523-14	Sequence 14, App
38	11	1.7	11	6	5196523-18	Sequence 18, App
39	11	1.7	18	6	5196523-17	Sequence 17, App
40	11	1.7	129	6	5196523-10	Sequence 10, App
41	10	1.6	10	6	5196523-16	Sequence 16, App
42	10	1.6	41	6	5196523-6	Sequence 6, App
43	10	1.6	41	6	5196523-6	Sequence 6, App
44	10	1.6	307	4	US-08-868-207A-481	Sequence 481, App
45	10	1.6	471	1	US-08-203-905B-2	Sequence 2, App1

ALIGNMENTS

RESULT 1
US-08-441-139-14
Sequence 14, Application US/08441139
Patent No. 5773245

GENERAL INFORMATION:
APPLICANT: MILEPHE, DR. KAZU D.
INVENTOR: MILEPHE, DR. KAZU D.
TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSER: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: NY
COUNTRY: USA
ZIP: 11530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENTLY USED FOR: Patent In Release #1.0, Version #1.25

CLASSIFICATION: A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,997
FILING DATE: 08-JUL-1993
NAME: DISCLOSURE
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8646
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 801 SANS UR
INVOICE NUMBER: 142
SEQUENCE CHARACTERISTICS: 14:
LENGTH: 646 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
US-08-441-139-14

Query Match 8.3%: Score 53; DB 1; Length 646;
Best Local Similarity 100.0%; Pred. No. 36-45;
Matches 53; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

QY 8 GIDLCCTTCVGVYFGKGVETIANDGNGNRTTPSYAVFTDTERLIDGAKNOVA 60

```

Db      8 GIDIGTTTSCVGFQKHVEIIANDQGNRTTSSVAFDTERLIGDANNOVA 60
|||||
RESULT 2
US-09-513-783A-174
; Sequence 174, Application US/09513783A
; Patent No. 6416959
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; INVENTOR: Caputo, Ray
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-11
; CURRENT APPLICATION NUMBER: US/09/513,783A
; CURRENT FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 174
; TYPE: DNA
; LENGTH: 180
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GFP-HSCTO
US-09-513-783A-174
Query Match      8.3% Score 53; DB 4; Length 890;
Best Local Similarity 100.0%; Pred. No. 4, 2e-45;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Oy      8 GIDIGTTTSCVGFQKHVEIIANDQGNRTTSSVAFDTERLIGDANNOVA 60
|||||
Db      232 GIDIGTTTSCVGFQKHVEIIANDQGNRTTSSVAFDTERLIGDANNOVA 304
|||||
RESULT 3
US-08-797-358B-3
; Sequence 3, Application US/08797358B
; Patent No. 6268478
; GENERAL INFORMATION:
; APPLICANT: Adams, John
; INVENTOR: Adams, John
; TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN
; FILE REFERENCE: 97-022-11
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,358B
; FILING DATE: 12-FEB-1997
; CLASSIFICATION: C08K000040
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,491
; FILING DATE: 12-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION/DOCKET NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-OE 3165
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 643 amino acids
; TYPE: amino acid
; SYNOBNESS: unknown

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; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-797-358B-3
Query Match      7.3% Score 47; DB 4; Length 643;
Best Local Similarity 100.0%; Pred. No. 3, 9e-39;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Oy      440 IOVYESERAMTKNNMLGFETLSGTPAPRGVQTEVTFDIANKIL 486
|||||
Db      442 IOVYESERAMTKNNMLGFETLSGTPAPRGVQTEVTFDIANKIL 486
|||||
RESULT 4
US-08-928-692-52
; Sequence 52, Application US/08928692
; Patent No. 5958727
; GENERAL INFORMATION:
; ADDRESSER: Brody, Howard
; APPLICANT: Brody, Howard
; APPLICANT: Lamsa, Michael
; TITLE OF INVENTION: Methods for Modifying the Production of
; TITLE OF INVENTION: a Polypeptide
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS: 710 No. 5958727disk of No. 5958727th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM compatible
; SOFTWARE: FASTSBO for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,692
; FILING DATE: 12-SEPT-1997
; CLASSIFICATION: C08K000040
; ADDRESSER: Lamsa, Michael
; NAME: Lamsa, Michael
; REGISTRATION/DOCKET NUMBER: 33,728
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: NO. 5958727e
US-08-928-692-52
Query Match      4.4% Score 28; DB 2; Length 339;
Best Local Similarity 100.0%; Pred. No. 4, 6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Oy      214 DGIFEVKATAGDTHLGGEGFQNLVNFH 241
|||||
Db      211 DGIFEVKATAGDTHLGGEGFQNLVNFH 238
|||||
RESULT 5
US-09-339-972-52
; Sequence 52, Application US/09339972
; Patent No. 6323002
; GENERAL INFORMATION:
; APPLICANT: Brody, Howard

```

? APPLICANT: Yaver, Deborah S.
 ? APPLICANT: Lamsa, Michael
 ? APPLICANT: Hansen, Kim
 ? TITLE OF INVENTION: Methods for Modifying the Production of
 ? POLYPEPTIDES
 ? NUMBER OF SEQUENCES: 180
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: No. 6323002a No. 6323002a disk of No. 6323002th America, Inc.
 ? STREET: 405 Lexington Avenue
 ? CITY: New York
 ? STATE: NY
 ? COUNTRY: USA
 ? ZIP: 10174
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Diskette
 ? COMPUTER: IBM Compatible
 ? OPERATING SYSTEM: DOS
 ? SOFTWARE: FASTSD for Windows Version 2.0
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/09/339,972
 ? FILING DATE:
 ? PRIORITY:
 ? CLASSIFICATION:
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: 08/928,692
 ? FILING DATE:
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Lambdis, Elias J
 ? REGISTRATION NUMBER: 33,728
 ? TELEPHONE: 212-867-0123
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 212-878-9655
 ? TELEFAX: 212-878-9655
 ? INFORMATION FOR SEQ ID NO: 52:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 339 amino acids
 ? STRANDNESS: single
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: No. 6323002e
 ? US-09-339-972-52
 ?
 ? Query Match 4.4%; Score 28; DB 4; Length 339;
 ? Best Local Similarity 100.0%; Pred. No. 4.6e-20;
 ? Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ? Oy 214 GSIPEYKATGCPHLCGSDPDNRLVNHF 241
 ? Db 211 GSIPEYKATGCPHLCGSDPDNRLVNHF 238
 ?
 ? RESULT 6
 ? US-09-214-583-2
 ? Sequence 2, Application US/08214583
 ? Patent No. 5627039
 ? GENERAL INFORMATION:
 ? APPLICANT: Pereira-Smith, Olivia
 ? APPLICANT: Madhwa, Renu
 ? TITLE OF INVENTION: MORTALIN AND METHODS FOR DETERMINING
 ? THE COMPLEMENTATION GROUP ASSIGNMENT OF CANCER CELLS
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Howrey & Simon
 ? STREET: 1299 Pennsylvania Ave, NW
 ? CITY: Washington
 ? STATE: DC
 ? COUNTRY: US
 ? ZIP: 20004
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patent Release #1.0, Version #1.25
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER:

? APPLICATION NUMBER: US/08/214,583
 ? FILING DATE:
 ? CLASSIFICATION: 435
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Amerbach, Jeffrey T
 ? REGISTRATION NUMBER: 33,728
 ? TELEPHONE: 202-383-7451
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 202-383-7451
 ? TELEFAX: 202-383-6610
 ? INFORMATION FOR SEQ ID NO: 2:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 679 amino acids
 ? STRANDNESS: single
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: protein
 ? HYPOTHETICAL: NO
 ? ORIGINAL SOURCE:
 ? ORGANISM: Murine
 ? IMMEDIATE SOURCE:
 ? CLONE: mortalin
 ? US-08-214-583-2
 ?
 ? Query Match 3.6%; Score 23; DB 1; Length 679;
 ? Best Local Similarity 100.0%; Pred. No. 1.1e-14;
 ? Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ? Oy 463 GIPAPRGVPIETVYDIDANGI 485
 ? Db 507 GIPAPRGVPIETVYDIDANGI 529
 ?
 ? RESULT 7
 ? US-08-257-073-7
 ? Sequence 7, Application US/08257073
 ? Patent No. 5786597
 ? GENERAL INFORMATION:
 ? APPLICANT: Rapolletti, Enzo
 ? APPLICANT: de Taisne, Charles
 ? TITLE OF INVENTION: MALARIA RECOMBINANT POXYVIRUS VACCINE
 ? NUMBER OF SEQUENCES: 143
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Cutlis, Morris & Safford, P.C.
 ? STREET: 300 15th Avenue, 25th Floor
 ? CITY: New York
 ? STATE: New York
 ? COUNTRY: UNITED STATES OF AMERICA
 ? ZIP: 10036
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patent Release #1.0, Version #1.30
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/257,073
 ? FILING DATE: 09-JUN-1994
 ? CLASSIFICATION: 424
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US 08/075,783
 ? PRIOR APPLICATION DATA: 1993
 ? APPLICATION NUMBER: US 07/852,305
 ? FILING DATE: 18-MAR-1992
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US 07/672,183
 ? FILING DATE: 20-MAR-1991
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Cutlis, Morris & Safford, P.C.
 ? REGISTRATION NUMBER: 33,728
 ? TELEPHONE: 212-506
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (212) 840-3333

TELEFAX: (212) 840-0712
 TELEX: 425066 CURTMS
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 315
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal
 US-08-257-073-7

Query Match 3.1%; Score 20; DB 1; Length 315;
 Best Local Similarity 100.0%; Pred. No. 66-12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 471 VPPIEVTFPIDANGILNVT 490
 DB 118 VPIEVTFPIDANGILNVT 137

RESULT 8

US-09-066-047-5
 Sequence 5, Application US/0906047A
 Patent No. 6506394

GENERAL INFORMATION:
 APPLICANT: BENTZ, Cheryl
 ATTORNEY/AGENT INFORMATION:
 BENTZ, Gerald A.
 COUSHLIN, Richard T.

TITLE OF INVENTION: NUCLEIC ACIDS, PROTEINS, AND METHODS OF
 USE OF GRANULOCYTIC EHRILICHA

NUMBER OF SEQUENCES: 41
 CORRESPONDENCE ADDRESS:
 STREET: 60 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: United States
 ZIP: 02109

COMPUTER READABLE FORM:
 COMPUTER TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/066,047A
 FILING DATE: 24-Apr-1998
 CLASSIFICATION: <unknown>
 PRIORITY INFORMATION:
 APPLICATION NUMBER: US 60/044,869
 FILING DATE: 25-APR-1997

ATTORNEY/AGENT INFORMATION:
 NAME: Superko, Colleen
 REGISTRATION NUMBER: 39,850
 REFERENCE/DOCKET NUMBER: 106,941,156
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 526-5000
 TELEFAX: (617) 526-5000

INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 649 amino acids
 TYPE: amino acid
 STRANDEDNESS: <unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal

US-09-066-047-5
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Query Match 3.0%; Score 19; DB 4; Length 649;
 Best Local Similarity 100.0%; Pred. No. 1.36-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 467 APAGVPIEVTFPIDANGI 485
 DB 463 APAGVPIEVTFPIDANGI 481

RESULT 9

US-08-240-514-37
 Sequence 37, Application US/08240514
 Patent No. 5670347

GENERAL INFORMATION:
 APPLICANT: GOPAL, T. Venkat
 ATTORNEY/AGENT INFORMATION:
 TITLE OF INVENTION: PEPTIDE-MEDIATED GENE TRANSFER
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA

COMPUTER READABLE FORM:
 COMPUTER TYPE: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/240,514
 FILING DATE: 1998-07-13
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 73521/102/CLIN

REFERENCE/DOCKET NUMBER: 73521/102/CLIN
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)672-5399
 TELEFAX: 904136

INFORMATION FOR SEQ ID NO: 37:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-240-514-37
 Query Match 2.8%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.9e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 245 FPKRKKKIDSONKRAVR 262
 DB 1 FPKRKKKIDSONKRAVR 18

RESULT 10

US-08-612-302A-37
 Sequence 37, Application US/08612302A
 Patent No. 5811297

GENERAL INFORMATION:
 APPLICANT: GOPAL, T. Venkat
 ATTORNEY/AGENT INFORMATION:
 TITLE OF INVENTION: PEPTIDE-MEDIATED GENE TRANSFER
 NUMBER OF SEQUENCES: 56
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Rattner & Prestia
 STREET: 1000 Pennsylvania Avenue, N.W.
 CITY: Valley Forge
 STATE: Pennsylvania
 COUNTRY: USA

COMPUTER READABLE FORM:
 COMPUTER TYPE: IBM PC compatible


```

/ OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/   PATENT NO.: 6380370
/   FILING DATE: 05/08/612.302A
/   CLASSIFICATION: 424
/   ATTORNEY/AGENT INFORMATION:
/     NAME: Amzel, Viviana
/     REGISTRATION NUMBER: 30,930
/     REFERENCE/DOCKET NUMBER: AMAA-020
/     TELECOMMUNICATION INFORMATION:
/       TELEPHONE: (610) 407-0700
/       TELEFAX: (610) 407-0701
/       TELEX: n.a.
/     TOPOLOGIES: n.a.
/ US-08-612-502A-37

Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 245 FKKRKKDJSOKRAVER 262
Db 1 FKKRKKDJSOKRAVER 18

RESULT 11
US-09-134-001C-3646
/ Sequence 3646, Application US/09134001C
/ Patent No. 6380370
/ GENETIC INFORMATION:
/   APPLICANT: Epidermidis-Stamm et al
/   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
/   FILE REFERENCE: GTC-007
/   CURRENT APPLICATION NUMBER: US/09/134,001C
/   PRIOR APPLICATION NUMBER: US 60/064,964
/   PRIOR FILING DATE: 1997-08-14
/   PRIOR FILING DATE: 1997-08-14
/   NUMBER OF SEQ ID NOS: 5674
/   SEQ ID NO 3646
/   LENGTH: 616
/   TYPE: PRT
/ ORGANISM: Staphylococcus epidermidis
/ US-09-134-001C-3646

Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 464 IPAPAPQJIEVTDID 481
Db 439 IPAPAPQJIEVTDID 456

RESULT 12
US-09-632-538C-36
/ Sequence 36, Application US/09632538C
/ Patent No. 6440674
/ GENETIC INFORMATION:
/   APPLICANT: Mistrant, Santosh et al
/   TITLE OF INVENTION: PLANT PROMOTER DERIVED FROM LUMINAL BINDING PROTEIN GENE AND METHOD
/   FILE REFERENCE: 54359
/   CURRENT APPLICATION NUMBER: US/09/632,538C
/   CURRENT FILING DATE: 2000-08-04

```

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/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 36
/ LENGTH: 655
/ US-09-632-538C-36
/ ORGANISM: Pseudotsuga menziesii

Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 461 LSPAPAPQJIEVTF 478
Db 483 LSPAPAPQJIEVTF 500

RESULT 13
US-08-480-190-132
/ Sequence 132, Application US/08480190
/ Patent No. 3623516
/ GENETIC INFORMATION:
/   APPLICANT: Robert G. Urban
/   APPLICANT: Roman M. Chicz
/   APPLICANT: Dario A. A. Vignali
/   APPLICANT: Mary L. Hedley
/   APPLICANT: Lawrence J. Stern
/   APPLICANT: Jack L. Strominger
/   TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
/   NUMBER OF SEQ ID NOS: 274
/   CORRESPONDENCE ADDRESS:
/     ADDRESSEE: Fish & Richardson
/     STREET: 225 Franklin Street
/     CITY: Boston
/     STATE: Massachusetts
/     COUNTRY: U.S.A.
/     ZIP: 02110-3980
/ COMPUTER READABLE FORM:
/   MEDIUM TYPE: 3.5" Diskette, 1.44 MB
/   COMPUTER: IBM PS/2 Model 502 or 555X
/   OPERATING SYSTEM: MS-DOS (Version 5.0)
/   SOFTWARE: WordPerfect (Version 5.1)
/   CURRENT APPLICATION DATA:
/     APPLICATION NUMBER: US/08/480,190
/     CLASSIFICATION: 424
/     PRIOR APPLICATION DATA:
/       APPLICATION NUMBER: 08/077,255
/       FILING DATE: June 15, 1993
/       APPLICATION NUMBER: 07/925,460
/       FILING DATE: August 11, 1992
/     ATTORNEY/AGENT INFORMATION:
/       NAME: Fish & Richardson
/       REGISTRATION NUMBER: 30,162
/       REFERENCE/DOCKET NUMBER: 00246/168001
/       TELECOMMUNICATION INFORMATION:
/         TELEPHONE: (617) 542-5070
/         TELEFAX: (617) 542-8906
/         TELEX: 200154
/       INFORMATION FOR SEQ ID NO: 132:
/         TYPE: amino acid
/         STRANDEDNESS:
/         LENGTH: 117
/         SEQUENCE CHARACTERISTICS:
/           TOPOLOGY: linear
/           US-08-480-190-132

Query Match
Best Local Similarity 100.0%; Pred. No. 3.8e-10;
Matches 17: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 38 TPSPYAFDFRLGDA 54
Db 1 TPSPYAFDFRLGDA 54

```

Db 1 TFSYVAFDTFRILGDA 17

RESULT 14

US-08-488-379-132

Sequence 132, Application US/08488379

Patent No. 5880103

GENERAL INFORMATION:

APPLICANT: Robert G. Urban

APPLICANT: Roman M. Chicz

APPLICANT: Mario A. A. Vignall

APPLICANT: Joseph J. Stier

APPLICANT: Lawrence J. Stern

APPLICANT: Jack L. Strominger

TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES

NUMBER OF SEQUENCES: 274

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB

COMPUTER: IBM PS/2 Model 502 or 555X

SOFTWARE: SIFT, FASTA, GDS (Version 5.0)

CURRENT APPLICATION DATA: (Version 5.1)

APPLICATION NUMBER: US/08/488,379

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/077,255

ATTORNEY/AGENT INFORMATION: 1592

APPLICATION NUMBER: 07/925,460

FILING DATE: August 11, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00246/168001

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 132:

SEQUENCE CHARACTERISTICS:

LENGTH: 17

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-488-379-132

Query Match 2.7%; Score 17; DB 2; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.8e-10;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 38 TFSYVAFDTFRILGDA 54

Db 1 TFSYVAFDTFRILGDA 17

RESULT 15

PCT-US93-07545-132

Sequence 132, Application PC/TUS9307545

GENERAL INFORMATION:

APPLICANT: Robert G. Urban

APPLICANT: Roman M. Chicz

APPLICANT: Mario A. A. Vignall

APPLICANT: Joseph J. Stier

APPLICANT: Lawrence J. Stern

APPLICANT: Jack L. Strominger

TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES

NUMBER OF SEQUENCES: 273

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB

COMPUTER: IBM PS/2 Model 502 or 555X

SOFTWARE: SIFT, FASTA, GDS (Version 5.0)

CURRENT APPLICATION DATA: (Version 5.1)

APPLICATION NUMBER: PCT/US93/07545

FILING DATE: 19930811

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/925,460

ATTORNEY/AGENT INFORMATION: 1592

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00246/168001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 132:

SEQUENCE CHARACTERISTICS:

LENGTH: 17

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

PCT-US93-07545-132

Query Match 2.7%; Score 17; DB 5; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.8e-10;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 38 TFSYVAFDTFRILGDA 54

Db 1 TFSYVAFDTFRILGDA 17

Search completed: December 4, 2002, 16:53:35

Job time : 18 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 16:35:46 : Search time 14 seconds

(without alignments)

1899.023 Million cell updates/sec

Title: US-09-646-835-1

Sequence: 1 MAAAALIGIDCTTSCGV.....FGAGFGKSGSGSPFIEVD 641

Scoring table: GAPOP 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3263	100.0	641	1 HS71_HUMAN	P08107 homo sapien
2	3225	98.8	641	1 HS72_BOVIN	Q27965 bos taurus
3	3216	98.6	641	1 HS71_BOVIN	Q27975 bos taurus
4	3186	97.3	641	1 HS71_PIG	Q34730 sus scrofa
5	3185	97.3	641	1 HS71_PIG	Q34730 sus scrofa
6	3148.5	96.5	638	1 HS71_CEREAL	Q08923 ratu
7	3130	95.9	641	1 HS71_MOUSE	P17879 mus musculus
8	2921	89.5	641	1 HS71_HUMAN	P34931 homo sapien
9	2887	88.5	641	1 HS71_MOUSE	P16627 mus musculus
10	2882	88.3	641	1 HS71_PIG	P55063 ratu
11	2862.5	87.7	646	1 HS7C_MOUSE	P08109 mus musculus
12	2851.5	87.5	650	1 HS7C_MOUSE	P11142 homo sapien
13	2843.5	87.1	646	1 HS7C_CEREAL	P19378 citriculus
14	2835.5	86.9	647	1 HS70_XENILA	P02827 xenopus lae
15	2816	86.3	651	1 HS70_ONCERY	P08108 oncohyranio
16	2812	86.2	649	1 HS7C_BARRA	Q09473 brachyranio
17	2810.5	86.1	644	1 HS70_ONCETS	Q91233 oncohyranio
18	2798	85.7	644	1 HS7C_PIG	Q04967 sus scrofa
19	2796	85.7	644	1 HS7C_PIG	Q04967 sus scrofa
20	2792.5	85.3	632	1 HS7C_MOUSE	Q08933 manduca sex
21	2776	85.1	649	1 HS7C_MOUSE	P47773 localuina
22	2776	85.1	649	1 HS7C_MOUSE	P47773 localuina
23	2772.5	85.0	639	1 HS72_HUMAN	P54653 homo sapien
24	2766	84.8	639	1 HS72_HUMAN	Q91291 pleurodeles
25	2762	84.6	634	1 HS70_CHICK	P08106 gallus galli
26	2755.5	84.4	633	1 HS72_RAT	P17855 ratu
27	2754.5	84.4	633	1 HS72_MOUSE	P17855 ratu
28	2737	83.6	651	1 HS70_MOUSE	P17855 ratu
29	2737	83.6	651	1 HS70_MOUSE	P17855 ratu
30	2735	83.8	644	1 HS70_BOVINA	P27541 brugia mala
31	2697.5	82.7	631	1 HS72_BOVIN	P34933 bos taurus
32	2678.5	82.1	686	1 HS7C_ORYZA	Q05691 oryza lat
33	2670.5	81.8	654	1 HS70_HYDRA	Q05944 hydra magni

ALIGNMENTS

RESULT 1	HS71_HUMAN	STANDARD:	PF:	641 AA.
ID	HS71_HUMAN	P08107	P18790, Q90080, Q90010,	
DC	P08107	P18790, Q90080, Q90010,		
DT	01-FEB-1994 (Ref. 28)			
DE	15-JUN-2002 (Ref. 41, Last annotation update)			
OS	Heat shock 70 kDa protein 1 (HSP70.1) (HSP70-1/HSP70-2).			
GN	(HSP70.1 OR HSP70.1) AND HSP70.1.			
OC	Homo sapiens (Human).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OR	11			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE:91055806; PubMed:1700760;			
RT	Malher C.M., Campbell R.D.;			
RL	"Structure and expression of the three MHC-linked HSP70 genes. "			
RM	Immunogenetics 32:242-251(1990).			
RX	SEQUENCE FROM N.A.			
RX	MEDLINE:96016721; PubMed:3931075;			
RT	Hunt C., Morimoto R.I.;			
RL	"Conserved features of eukaryotic hsp70 genes revealed by comparison with the nucleotide sequence of human hsp70. "			
RM	Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).			
RX	SEQUENCE FROM N.A. (HSP70.1 AND HSP70.1).			
RX	Malher C.M., Campbell R.D.;			
RA	Abassi N., Dickhof R., Loretz C., Maden A., Dore M., Young J.,"			
RL	Laissy S., Hood L.;			
RM	"Sequence of the human major histocompatibility complex class III region. "			
RL	Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.			
RX	SEQUENCE FROM N.A. (HSP70.1 AND HSP70.1).			
RX	Malher C.M., Durrum I., Frowde J., Campbell R.D.;			
RA	Shih S., Tamay G., Oka A., Inoko H.;			
RL	"Homo sapiens 2,329,817bp genomic DNA of 6p21.3 HLA class I region. "			
RM	Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.			
RX	SEQUENCE OF 1-36 AND 360-424 FROM N.A.			
RX	MEDLINE:99184548; PubMed:2538825;			
RA	Sargent C.A., Durrum I., Frowde J., Campbell R.D.;			
RL	human major histocompatibility complex contains genes for the major histocompatibility complex class I region. "			
RM	Proc. Natl. Acad. Sci. U.S.A. 86:1966-1972(1989).			
RX	SEQUENCE OF 1-22 AND 618-641 FROM N.A.			
RX	MEDLINE:87066768; PubMed:3766141;			
RA	Drabant B., Gentile A., Benke B.-J.;			
RL	in vitro transcription of a human hsp 70 heat shock gene by extracts from heat-shocked human cells. "			
RM	Nucleic Acids Res. 14:9833-9849(1986).			
RL	[7]			
RX	X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-382.			
RX	MEDLINE:99234376; PubMed:10216320;			

P29843 drosophila
P09446 caenorhabdi
P08418 schistosoma
P41827 anopheles a
Q01877 anopheles a
P41825 anopheles a
P09189 peritoma hyb
Q10265 schizosacch
P22953 arabidopsis
P82910 drosophila
P02824 drosophila


```

CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CC CONFORMATION OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
CC SEQUENCES WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CC DURING TRANSLATION AND MEMBRANE TRANSLLOCATION, OR FOLLOWING
CC STRESS-INDUCED DAMAGE.
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
CC EMBL: 0028923; AAA05451.1; -
CC EMBL: M98823; AAA30568.1; -
CC HSP70; P08107; H70; -
CC HSP70; P08107; H70; -
CC HSP70; P08107; H70; -
CC PRINTS: PR00301; HEATSHOCK70.
CC PRODOM: PD000089; HSP70_1; -
CC PROSITE: PS00297; HSP70_1; 1.
CC PROSITE: PS00329; HSP70_2; 1.
CC PROSITE: PS01036; HSP70_3; 1.
CC APP-BINDING: Chaperone; Heat shock; Multigene family.
CC SEQUENCE 641 AA: 70228 MW: 22901968610DF CRC64:
CC -----
Query Match 98.8%; Score 3225; DB 1; Length 641:
Best Local Similarity 98.7%; Pred. No. 1;e-171;
Matches 634; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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CC 601 QVCPNPTISLYOGAGPGGPGGAGGPGKGGSSGPTLEVD 641
CC ||||||| ||||||| ||||||| ||||||| |||||||
CC 601 QVCPNPTISLYOGAGPGGPGGAGGPGKGGSSGPTLEVD 641
CC -----
CC RESUME 3
CC ID HSP71_BOVIN STANDARD: PRT: 641 AA.
CC Q27975; Q27964;
CC 01-NOV-1997 (Rel. 35, Created)
CC 15-JUL-1999 (Rel. 35, Last sequence update)
CC 15-JUL-1999 (Rel. 38, Last annotation update)
CC HSP71 shock 70 kDa protein 1 (HSP70-1).
CC Bos taurus (Bovine).
CC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC Bovidae; Bovine; Bos.
CC NCBI-TaxID=9913;
CC (1)
CC SOURCE FROM N.A.
CC REF: HSP71_BOVIN; PubMed:782632;
CC Gettier J.A., Guerrero V.;
CC "Chemical modifications of a recombinant bovine stress-inducible 70
CC kDa heat-shock protein (HSP70) mimics Hsp70 isoforms from tissues."
CC Biochem. J. 305:197-203 (1995).
CC [2]
CC SEQUENCE OF 212-641 FROM N.A.
CC REF: HSP71_BOVIN; PubMed:7943958;
CC MEDLINE=95030563; PubMed=7943958;
CC Grosz M.D., Skow L.C., Stone R.T.;
CC "An Alu polymorphism at the bovine 70 kD heat-shock protein-1
CC (HSP70-1) locus."
CC Anim. Genet. 25:196-196 (1994).
CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
CC PREEXISTING PROTEINS AGAINST AGGREGATION AND MODULATE THE FOLDING
CC OF NEWLY SYNTHESIZED POLYPEPTIDES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC
CC RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR
CC PROTEIN TRANSLLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
CC PATHWAYS IN COOPERATION WITH HSP90. THEY PARTICIPATE IN ALL THESE
CC PROCESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE
CC CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE
CC SEQUENCES WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES
CC DURING TRANSLATION AND MEMBRANE TRANSLLOCATION, OR FOLLOWING
CC STRESS-INDUCED DAMAGE.
CC -1- INDUCTION: BY HEAT SHOCK.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
CC EMBL: 009861; AAA73914.1; -
CC EMBL: M98823; AAA30568.1; -
CC HSP70; P08107; H70; -
CC HSP70; P08107; H70; -
CC Pfam: PF001023; HSP70.
CC PRINTS: PR00301; HEATSHOCK70.
CC PRODOM: PD000089; HSP70_1; -
CC PROSITE: PS00297; HSP70_1; 1.
CC PROSITE: PS00329; HSP70_2; 1.
CC PROSITE: PS01036; HSP70_3; 1.
CC APP-BINDING: Chaperone; Heat shock; Multigene family.
CC SEQUENCE 641 AA: 70230 MW: 625482635878099 CRC64:
CC -----
Query Match 98.8%; Score 3216; DB 1; Length 641:
Best Local Similarity 98.8%; Pred. No. 3;e-171;

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RESULT 5
 HS7L_CERAE STANDARD; PRT: 641 AA.
 AC 027139
 DT 01-SEP-1995 (Rel. 31, Created)
 DT 01-SEP-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Heat shock 70 kDa protein 1/2 (HSP70.1/2).
 GN HSP70-1 AND HSP70-2.
 OS Rattus norvegicus (Rat).
 OC Mammalia; Metazoa; Chordata; Craniata; Euteleostomi;
 OC OC; Mammalia; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxId=10116;
 (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=94096443; PubMed=8271311;
 RA Longo F.M., Wang S., Narasimhan P., Zhang J.S., Chen J.,
 RA Massa S.K., Sharp F.R.;
 RT Heat shock 70 gene expression of stress-inducible rat hsp70 in normal
 RT and injured rat brain.
 RL J. Neurosci. Res. 36:325-335(1993).
 (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=LEM 1W/GUN;
 RX MEDLINE=95012453; PubMed=7927556;
 RA Walter L., Raah F., Guenther E.;
 RT Heat shock 70 gene expression of a major histocompatibility complex-
 RT linked heat shock protein 70 (Hsp70) genes of the rat.*;
 RL Immunogenetics 40:325-330(1994).
 (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=94368874; PubMed=8085419;
 RA Kozlowski Z., Malicki P., Wolniczka P., Mastelowski J.;
 RT Cloning nucleotide sequence and expression of rat heat inducible
 RT hsp70 gene.*;
 RL Blochim. Biophys. Acta 1219:64-72(1994).
 CC -1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
 CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDIANE THE FOLDING
 CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
 CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES
 CC THROUGHOUT THE CELL CYCLE. IN ADDITION, THEY ARE INVOLVED IN
 CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEQUENCES WITH NER-
 CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION
 CC AND MEMBRANE TRANSLLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.
 CC -1- INDUCTION: BY HEAT SHOCK.
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
 CC
 CC THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration
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 CC
 CC EMBL: X72208; AAA14431.1;
 CC EMBL: X72208; AAA14431.1;
 CC EMBL: X72207; CAA54422.1;
 CC EMBL: X74271; CAA53238.1;
 CC HSP70; P08107; IAH0.
 CC InterPro: IPR001023; HSP70.
 CC Pfam: PF00012; HSP70.1;
 CC PRINTS: PF00302; HEATSHOCK70.
 CC PROSITE: PS00297; HSP70.1.1;
 CC PROSITE: PS00329; HSP70.2.1;
 CC PROSITE: PS01036; HSP70.3.1;
 CC ATP-binding; Chaperone; Heat shock; Multigene family.
 CC CONFLICT 71 72 D -> NG (IN REF. 3).
 CC CONFLICT 227 227 R -> H (IN REF. 2 AND 3).

FT CONFLICT 408 408 G -> A (IN REF. 3).
 SQ SEQUENCE 641 AA: 70159 MW: 70159.6751C686583 CRC64;
 Query Match 96.8%; Score 3160; DB 1; Length 641;
 Best Local Similarity 96.4%; Pred. No. 4,4e-168;
 Matches 616; Conservative 15; Mismatches 10; Indels 0; Gaps 0;
 1 MAANAAGICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 21 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 31 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 41 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 51 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 61 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 71 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 81 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 91 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 101 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 111 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 121 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 131 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 141 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 151 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 161 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 171 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 181 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 191 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 201 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 211 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 221 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 231 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 241 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 251 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 261 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 271 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 281 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 291 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 301 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 311 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 321 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 331 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 341 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
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 381 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
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 411 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 421 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 431 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 441 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 451 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 461 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 471 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 481 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 491 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 501 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 511 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 521 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
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 561 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 571 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 581 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 591 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 601 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 611 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 621 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 631 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 641 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 651 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 661 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 671 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 681 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 691 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 701 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 711 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 721 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 731 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 741 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 751 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 761 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 771 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 781 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
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 811 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 821 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 831 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 841 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 851 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 861 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 871 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 881 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 891 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 901 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 911 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 921 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 931 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 941 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 951 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 961 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 971 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 981 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 991 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60
 1001 1 MARKKAAICIDGTTTCYSCVQVQHKVEILIANDGKRRFTTSVAVFDTRILIDMAKNQVA 60

D6	478	DANGILWAVADPDSYSGANKKTTINDKSRSLSEELRNVOVEAEKYAADVDEPRFSAAN
Qy	541	ALESTAFNKNASVAEDIEIKGRLISKISEDAKKRYDKDCOEVI SMLDANTLALKEOFERHRELF
D6	538	ALSTAFNKNASVAEDIEIKGRLISKISEDAKKRYDKDCOEVI SMLDANTLALKEOFERHRELF
Qy	601	QVONCFNISGLVGAGCGPGGAGACGGPGSSGSCPTFEVD 641
D6	598	QVONCFNISGLVGAGCGPGGAGACGGPGSSGSCPTFEVD 638
<hr/>		
hs717 mouse		
ID	HS717_MOUSE	STANDARD:
PRT:	641 AA.	
AC	P17879; MOE1689;	
DT	01-NOV-1990 (Rel. 15, Created)	
DT	01-NOV-1997 (Rel. 35, Last sequence update)	
DT	16-OCT-2001 (Rel. 40, Last annotation update)	
DR	HSP70_HUMAN	Heat shock protein 1 (HSP70.1) (HSP70.1/HSP70.2).
OS	Homo sapiens	(Human)
OS	Mus musculus (Mouse)	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Euarchontoglires; Rodentia; Sciurognathi; Muridae; Mus;	
NCBI_TaxId	10090;	
RN	[1]	
RN	SEQUENCE FROM N.A.	
RX	MEDLINE:06-0216310; PubMed:2321619;	
RC	TISSUE= Liver;	
RC	PubMed:94357449; PubMed:8076831;	
RT	Protein	
RT	Structure and expression of an inducible hsp70-encoding gene from	
RT	Mus musculus .	
RT	Gene 146:272-278(1994).	
CC	- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE	
CC	PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDiate THE FOLDING	
CC	OF MEMBRANE TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS THE NUCLEAR	
CC	THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATION OF	
CC	OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET	
CC	HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION	
CC	AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.	
CC	- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.	
CC	-----	
CC	This Swiss-ProT entry is copyright. It is produced through a collabora-	
CC	tion between the European Bioinformatics Institute and the restrictions o-	
CC	n use by non-profit institutions as long as its content is in the public do-	
CC	mained and this statement is not removed. Usage by and for comm-	
CC	entities requires a license agreement (See http://www.lsb-sib.ch/amn	
CC	or send an email to license@lsb-sib.ch).	
CC	
CC	EMBL: M5621; AAA37284.1; -	
CC	PIR: JH0095; JH0095.	
CC	HSP: P08107; I4H05.	
DR	MCD; MG1:99517; Hsp70-1.	
DR	InterPro: IPRO01023; Hsp70.	
DR	Pfam: PF00012; Hsp70_1.	
DR	PRINTS: PR03010; HEATSHOCK70.	
DR	PROSITE: PS00297; HSP70.1.1	
DR	PROSITE: PS00329; HSP70.2.1	
DR	PROSITE: PS01036; HSP70.3.1	
KM	ATP-binding; Chaperone; Heat shock; Multigene family.	
FT	CONFLICT 342 342	
FT	P > R (IN REF. 1).	
FT	CONFLICT 627 627	

OY 422 TKGQITFTYSNDQPGVLIQVYBEERAKTKDNLLGRPELSGTPAPRGVQPIEVTFDID 481
 DB 424 PRCQIQTFTYSNDQPGVLIQVYBEERAKTKDNLLGRPELSGTPAPRGVQPIEVTFDID 483
 OY 482 ANGLINATATDKSTGKANKITTTNDGKSLKSPRIEFMVOAEKRYAEDVQREKSAANA 541
 DB 484 ANGLINATATDKSTGKANKITTTNDGKSLKSPRIEFMVOAEKRYAEDVQREKSAANA 543
 OY 542 LESTARPKMSAVEDGJLCKIISEAKKKVLDGCEYISMLDANTLAKDSEFERRELEID 601
 DB 544 LESTARPKMSAVEDGJLCKIISEAKKKVLDGCEYISMLDANTLAKDSEFERRELEID 603
 OY 602 VCNPIISGLYOGAGPGPGRGAGGAGSG-----SGPTIEVD 641
 DB 604 MCNPITIKLYOG-----GCTGACGCTGVYGGPRATGPTIEVD 641
 RESULT 9
 ID HS77 MOUSE STANDARD: PRT: 641 AA.
 AC P16627: 061693; (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 41, Last annotation update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CR Heat shock 70 kDa like protein 1.
 CR Heat shock 70 kDa like protein 1.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Mus.
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 (1)
 RN SEQUENCE FROM N.A.
 RA MEDLINE=9041773; PubMed=2302214;
 RT Cloning of a hsp70-related gene expressed in mouse spermatids.
 RL Biochem. Biophys. Res. Commun. 186:43-49(1990).
 (2)
 RN REVISIONS.
 RA Fujimoto H.:
 RA Submitted (XX-1995) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis.
 RA MEDLINE=9429928; PubMed=8026864;
 RA Snek W., Olavsen M.G., van Vugt H., Milner C.M., Teuscher C.,
 Campbell R.D.:
 RA "Coding sequences and levels of expression of Hsc70 are identical in
 mammalian different tissues."
 RL Immunogenetics 40:159-162(1994).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN SPERMATIDS.
 CC -1- DEVELOPMENTAL STAGE: SPECIFICALLY EXPRESSED IN POSTMEIOTIC PHASES
 CC OF SPERMATOGENESIS.
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation.
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 CC or send an email to license@isb-slb.ch).
 CC -----
 CC EMBL: M32218; AAA74906.1; --
 CC PIR: A34043; AAA95962.1; --
 CC PIR: A34043; AAA95962.1; --
 CC HSPB: P08107; JMO1.
 CC MGI: MGI-96231; Hspb11.
 CC InterPro: IPR010233; Hsp70.
 CC Pfam: PF00012; Hsp70.
 CC PRINTS: PF000301; HEATSHOCK70.
 CC PRODOM: PD000089; Hsp70_1.
 CC PROSITE: PS00297; Hsp70_1; 1.

DR PROSITE: PS00329; HSP70_2; 1.
 DR PROSITE: PS01036; HSP70_3; 1.
 DR ART-Abinding: Heat shock; Multigene family; Spermatogenesis.
 RN Accession: 641 AA; 70695 MW; 38CA1521780362A CMC64.
 SO SEQUENCE
 Query Match 88.5%; Score 2887; DB 1; Length 641;
 Best Local Similarity 89.0%; Pred. No. 5,9e-153;
 Matches 569; Conservative 32; Mismatches 36; Indels 2; Gaps 2;
 OY 3 KAAATGIDGTTSCVYVQKAKVEIINDCONNTFTSYAFDTDELLIGAKKNOVALN 62
 DB 5 KMAATGIDGTTSCVYVQKAKVEIINDCONNTFTSYAFDTDELLIGAKKNOVALN 64
 OY 63 PONTVVDKAKLIQKPCDYYVQSMKMPVQYINDQKPKVQYKGEFKAFPEELSSM 122
 DB 65 PONTVVDKAKLIQKPCDYYVQSMKMPVQYINDQKPKVQYKGEFKAFPEELSSM 124
 OY 123 VLTAKKEIAEALYIGTPYNAIVTVPRATNDSDQKQANVIAQNTLVINPTMAAIA 182
 DB 125 VLTAKKEIAEALYIGTPYNAIVTVPRATNDSDQKQANVIAQNTLVINPTMAAIA 184
 OY 183 YELDRKRGKGERNNYILFDLGGSTGDSVILITLDGJFEVANAAGDVLGGEDDMRLVHEV 242
 DB 185 YELDRKSGIERHYILFDLGGSTGDSVILITLDGJFEVANAAGDVLGGEDDMRLVHEV 244
 OY 243 EEFRRKKKKKDIQNKRNRLRACERAKRTLSSTQASLEDSLEFGIDPTYSITANR 302
 DB 245 EEFRRKKKKDIQNKRNRLRACERAKRTLSSTQASLEDSLEFGIDPTYSITANR 304
 OY 303 ERLISDLFRSTLEPEKALIRAKLDQKQIDHDLYVGGSTRIPKQKLDQFFNGSDLNKS 362
 DB 305 ERLCADLFRGTEPEKSLRQAKKQKATHDYLVGGSTRIPKQKLDQFFNGSDLNKS 364
 OY 363 IMPREANVAGAAVQALILMGKSEKVOYDILLDVAFLSLGELAGVYMLVLRNSTIP 422
 DB 365 IMPREANVAGAAVQALILMGKSEKVOYDILLDVAFLSLGELAGVYMLVLRNSTIP 424
 OY 423 KQTQITFTYSNDQPGVLIQVYBEERAKTKDNLLGRPELSGTPAPRGVQPIEVTFDID 482
 DB 425 KQTQITFTYSNDQPGVLIQVYBEERAKTKDNLLGRPELSGTPAPRGVQPIEVTFDID 484
 OY 483 NGILNATATDKSTGKANKITTTNDGSLKSPRIEFMVOAEKRYAEDVQREKSAANA 542
 DB 485 NGILNATATDKSTGKANKITTTNDGSLKSPRIEFMVOAEKRYAEDVQREKSAANA 544
 OY 543 LESTARPKMSAVEDGJLCKIISEAKKKVLDGCEYISMLDANTLAKDSEFERRELEID 602
 DB 545 LESTARPKMSAVEDGJLCKIISEAKKKVLDGCEYISMLDANTLAKDSEFERRELEID 604
 OY 603 CNPIISGLYOGAGPGPGRGAGGAGSG-----SGPTIEVD 641
 DB 605 CNPIITIKLYOG-----GCTGACGCTGVYGGPRATGPTIEVD 641
 RESULT 10
 ID HS73 RAT STANDARD: PRT: 641 AA.
 AC P51063;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 CR Heat shock 70 kDa protein 3 (HSP70.3).
 CR Hsp70-3.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Rattus.
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 (1)
 RN SEQUENCE FROM N.A.
 RA STRAIN=LEM 14/GUN.
 RA MEDLINE=95012453; PubMed=7927336;
 RA Walter L., Raub P., Gentsch E.;

	Query	88.3%	Score	2882.1	De-151	Length	641:			
	Best Local Similarity	88.0%	Pred.	No.	1e-155					
	Matches	569:	Conservative	32:	Mismatches	33:	Indels	8:	Gaps	3:
QY	3	KAAATGIDGATGTCYGVFQHKREVLIIANDGKRTTFSVAFPTDTERLIDGAKNOVALN	62							
DB	5	KGNATGIDGATGTCYGVFQHKREVLIIANDGKRTTFSVAFPTDTERLIDGAKNOVALN	64							
QY	63	PNQPNPKALIGKRGKQVQWQMKHPIVQVINGCKRPNQVYSGCTAAPEEISSM	124							
DB	65	PNQPNPKALIGKRGKENDPVQSGDKLMPHPIVQVINGCKRPNQVYSGCTAAPEEISSM	122							
QY	123	VTRKKELEPAVIGYPPVNAVITPAVAPNDQSQFQATDQVAGLNLVLRINPEPAAALA	182							
DB	125	VTRKKELEPAATLQSHVNAVITPAVAPNDQSQFQATDQVAGLNLVLRINPEPAAALA	184							
QY	183	YGLDRTGKGRWALPDJAGGTFEWSLITLDDGIEFYKATAGDHLGGEFPNKLNVHFV	242							
DB	185	YGLDRTGKGRWALPDJAGGTFEWSLITLDDGIEFYKATAGDHLGGEFPNKLNVHFV	244							
QY	243	EEFKRKHYSQKRAVARELPALCPAARPTSSSTQALSIQSLSECTDEFTSITRAAF	302							
DB	245	EEFKRKHYSQKRAVARELPALCPAARPTSSSTQALSIQSLSECTDEFTSITRAAF	304							
QY	303	EEICSLDFRSLTEVEFKALIDAKDCKRQHDVLVVGSGSTRIPYKVKLLOQFPNCDLNS	362							
DB	305	EEICSLDFRSLTEVEFKSLIDAKDRAKIHIVLVGSTRIPYKVKLLOQFPNCDLNS	364							
QY	363	INDEPAVATGAVALIMKDSKRWODLLDLQVAPSLGTEITAGVWALITKRNSTPT	422							
DB	365	INDEPAVATGAVALIMKDSKRWODLLDLQVAPSLGTEITAGVWALITKRNSTPT	424							
QY	422	KQVQFPTTSSDQGVLTQYVGBREAVFNDMLNLRDLDTGIPPAIRGQVQIETPTDA	484							
DB	425	KQVQFPTTSSDQGVLTQYVGBREAVFNDMLNLRDLDTGIPPAIRGQVQIETPTDA	484							
QY	483	KGLILNVYADQSTCKANLITINQKGLSKKELEFMVQVQKRYAADQVQRRYSANAL	542							
DB	485	KGLILNVYADQSTCKANLITINQKGLSKKELEFMVQVQKRYAADQVQRRYSANAL	544							

QY	543	ISFAFMKMSAVSDGKIKGSISEMDKKVYLDKOCYSIMLADTATLAEDFFHNRRL	604
DB	545	ISFAFMKMSAVSDGKIKGSISEMDKKVYLDKOCYSIMLADTATLAEDFFHNRRL	604
DB	603	CNPIITKYSOSCTGTCATC-----YTCGARTGIIETED	641
DB	605	CNPIITKYSOSCTGTCATC-----YTCGARTGIIETED	641
		RESULT 11	
		HS7C.MOUSE	STANDARD: PRT; 646 AA.
IC	HS7C.MOUSE	P08109; P12255; Q62373; Q62374; Q62375;	
ID	HS7C-1988	(Rel. 08, Created	
DI	01-AUG-1988	(Rel. 41, Last annotation update)	
DT	15-JUN-2002	(Rel. 41, Last annotation update)	
DR	Heat shock cognate 71 kDa protein.		
GN	HSPA8 OR HSCT0 OR HSCT3.		
OS	Mus musculus (Mouse), and		
OC	Rattus norvegicus (Rat).		
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
CC	1) Taxid=10090, 10116.		
PN	SEQUENCE FROM N.A.		
RC	SPECIES-BAT:		
RX	MEDLINE-87246537; Pubmed-3595567;		
RA	Scorer P.K., Pellham H.R.B.;		
RT	"Cloning and expression of a gene encoding hsc73, the major hep70-like		
RT	protein in unstressed rat cells.,"		
RL	PMO J. 6:395-396(1987).		
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RC	SPECIES-BAT:		
RX	MEDLINE-8610827; Pubmed-3595319;		
RA	O'Malley K., Mauron A., Barbach J.D., Kedes L.;		
RT	"Constitutively expressed rat mRNA encoding a 70-kilodalton heat-		
RT	shock-like protein.,"		
RL	Mol. Cell. Biol. 5:3476-3483(1985).		
RP	SEQUENCE FROM N.A.		
RC	SPECIES-MOUSE:		
RX	MEDLINE-9805872; Pubmed-334718;		
RA	Glebeil L.B., Dorniczak B.P., Bantz E.K.F.;		
RT	"Expression of a 70-kDa heat shock protein, constitutively expressed mouse mRNA		
RT	encoding a 72-kDa heat shock-like protein.,"		
RL	Dev. Biol. 125:200-207(1988).		
RP	SEQUENCE FROM N.A.		
RC	SPECIES-MOUSE:		
RX	MEDLINE-9310702; Pubmed-1037374;		
RA	Morhauser R.C., Hu W., Wang H., Pang Y., Flynn G.C.,		
RT	"High-resolution solution structure of the 18 kDa substrate-binding		
RT	domain of the 70-kDa heat shock cognate protein hsc70		
RL	Nucleic Acids Res. 18:6565-6571(1990).		
RP	SEQUENCE BY NMR OF 385-543.		
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RA	Morhauser R.C., Hu W., Wang H., Pang Y., Flynn G.C.,		
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RX	MEDLINE-9310702; Pubmed-1037374;		
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 AC P19120;
 DT 01-NOV-1990 (rel. 16. Created)
 DT 01-NOV-1990 (rel. 16. Last sequence update)
 DT 16-OCT-2001 (rel. 40. Last annotation update)
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 GN HSPAB OR HSC70.
 OS Bos taurus (Bovine).
 OC Buckyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovine; Bos.
 RX NCBI_TaxId=9913;
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 RX ISSUES=10016026; PubMed=2215746;
 RX MEDLINE=9014656; PubMed=2215746;
 RX Deluce-Plaherly C. Mckay D.B.;
 RX "The amino acid sequence of the cDNA of a bovine 70 kilodalton heat shock
 RX cognate protein.";
 RX Nucleic Acids Res. 18:5569-5569(1990).
 RN (2)
 RX X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 1-385.
 RX MEDLINE=90348961; PubMed=24143562;
 RX Deluce-Plaherly C. Mckay D.B.;
 RX "Three-dimensional structure of the ATPase fragment of a 70K
 RX heat-shock cognate protein.";
 RX Nature 346:623-628(1990).
 RN (3)
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 RX MEDLINE=94230372; PubMed=8175707;
 RX Deluce-Plaherly C. Mckay D.B.;
 RX "The amino acid sequence of the cDNA of a bovine 70 kilodalton heat shock cognate protein ATP
 RX hydrolytic activity. II: Structure of the active site with ADP or ATP
 RX bound to wild type and mutant ATPase fragment.";
 RX J. Biol. Chem. 269:12899-12907(1994).
 RN (4)
 RX X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-385.
 RX MEDLINE=96234532; PubMed=9585559;
 RX Deluce-Plaherly C. Mckay D.B.;
 RX "The amino acid sequence of the cDNA of a bovine 70 kilodalton heat shock cognate protein ATP
 RX hydrolytic activity. I: Structure of the active site monovalent cations by the
 RX epsilon-amino group of lysine in the ATPase fragment of bovine
 RX Hsc70.";
 RX Biochemistry 37:7456-7462(1998).
 RN (5)
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 RX MEDLINE=99017893; PubMed=9795500;
 RX Soula M.C., McKay D.B.;
 RX "The amino acid sequence of the cDNA of a bovine 70-kDa heat shock cognate
 RX protein is essential for transducing the ATP-induced conformational
 RX change.";
 RX Biochemistry 37:15392-15399(1998).
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 RX Deluce-Plaherly C. Mckay D.B.;
 RX "The amino acid sequence of the cDNA of a bovine 70-kDa heat shock cognate
 RX protein is essential for transducing the ATP-induced conformational
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 CC 1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
 CC "This Swiss-Prot entry is it is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL consortium."
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC EMBL: X53827; CAJ7823.1;
 CC EMBL: X53335; CAJ7422.1;
 CC PIR: S11456; S11456.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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3	162	15.9	162	10	US-09-761-3544-10	Sequence 10, April
4	264	1.0	264	10	US-09-864-761-35298	Sequence 36258, April
5	71	11.1	137	10	US-09-825-301-1519	Sequence 1519, April
6	53	8.3	646	9	US-09-870-759-43	Sequence 43, April
7	53	8.3	646	9	US-09-759-010-4	Sequence 4, April
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9	65.1	9	65.1	9	US-10-108-605-75	Sequence 75, April
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RESULT 2
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Sequence 36258, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Danzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DEIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecolca-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,5
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-02
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408

;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; PRIOR FILING DATE: 2001-01-29
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;; SEQ ID NO 36258
;; LENGTH: 168
;; TYPE: PRT
;; ORGANISM: Homo sapiens

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US-09-864-761-36258

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RESULT 3
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Sequence 10, Application US/09761534A
Patent No. US20020146436A1
GENERAL INFORMATION:
APPLICANT: Huang, Qian
APPLICANT: Richmond, Jean F.L.
APPLICANT: Rank, David R.
APPLICANT: Danzel, David R.
APPLICANT: Chen, Jianzhu
APPLICANT: Eisen, Herman N.
APPLICANT: Young, Richard A.
TITLE OF INVENTION: In Vivo CTL Elicitation By Heat Shock
TITLE OF INVENTION: Protein Fusion Proteins Maps To A Discrete Domain and Is
TITLE OF INVENTION: GDA+Cell-Independent
CURRENT APPLICATION NUMBER: US 09/761,534A
CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: PCT/US00/32831
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 60/176,143
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 23
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TYPE: PRT
ORGANISM: Unknown
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;; OTHER INFORMATION: Murine hsp70
US-09-761-534A-10

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Oy      138  PVTNATVTPAFENDSORATFDAGVIGLNLVLRITNEPTAALINAGCDPTGGRRWLLI 197
Db      138  PVTNATVTPAFENDSORATFDAGVIGLNLVLRITNEPTAALINAGCDPTGGRRWLLI 197
Oy      198  FDLGGFGFVSILTLIDGGIEFVKKATGSHLGGEDDNNLAV 238
Db      198  FDLGGFGFVSILTLIDGGIEFVKKATGSHLGGEDDNNLAV 238
Oy      198  FDLGGFGFVSILTLIDGGIEFVKKATGSHLGGEDDNNLAV 238
Db      198  FDLGGFGFVSILTLIDGGIEFVKKATGSHLGGEDDNNLAV 238

RESULT 4
US-09-761-534A-12
Sequence 12, Application US/09761534A
Patent No. US20020146426A1
GENERAL INFORMATION:
APPLICANT: Huang, Qian
APPLICANT: Richmond, Joan F.L.
APPLICANT: Cho, Bryan K.
APPLICANT: Ealliser, Deborah
APPLICANT: Elson, Judith N.
APPLICANT: Young, Richard A.
APPLICANT: Young, Richard A.
TITLE OF INVENTION: In Vivo CTL Proliferation By Heat Shock
TITLE OF INVENTION: Protein Fusion Proteins Maps To A Discrete Domain and Is
FILE REFERENCE: 0399, 2006-003
CURRENT FILING DATE: 2001-01-16
PRIORITY FILING DATE: 2000-12-01
PRIORITY FILING DATE: 2000-12-01
PRIORITY FILING DATE: 2000-12-01
PRIORITY FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 209
ORIGIN: DNA
ORIGIN: Unknown
FEATURE:
OTHER INFORMATION: Murine hap70 - Segment II
US-09-761-534A-12

Query Match      11.2%; Score 72; DB 10; Length 209;
Best Local Similarity 100.0%; Pred. No. 1.1e-60;
Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      240  HVEEPRKRRKKKIDSONRNVRLRFGCEAFRTSSSTOKSLFDSFEDPTGSTR 299
Db      240  HVEEPRKRRKKKIDSONRNVRLRFGCEAFRTSSSTOKSLFDSFEDPTGSTR 299
Oy      51  HFVEEPRKRRKKKIDSONRNVRLRFGCEAFRTSSSTOKSLFDSFEDPTGSTR 110
Db      51  HFVEEPRKRRKKKIDSONRNVRLRFGCEAFRTSSSTOKSLFDSFEDPTGSTR 110

Oy      300  ARFEELCSDFER 311
Db      300  ARFEELCSDFER 311
Oy      111  ARFEELCSDFER 122
Db      111  ARFEELCSDFER 122

RESULT 5
US-09-925-301-1519
Sequence 1519, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
CURRENT FILING DATE: 2001-08-10
CURRENT FILING DATE: 2001-08-10
CURRENT FILING DATE: 2001-08-10
CURRENT FILING DATE: 2000-03-08
PRIORITY FILING DATE: 2000-03-08
PRIORITY FILING DATE: 2000-03-08
PRIORITY FILING DATE: 1999-03-12

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? NUMBER OF SEQ ID NOS: 1694
? SOFTWARE: Patentin Ver. 2.0
Oy Db
? SEQ ID NO 119
? SEQ ID NO 117
? TYPE: PRT
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: SITE
? LOCATION: (772)
? OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1519
Query Match
Best Local Similarity 100.0%; Pred. No. 6-9e-60; Length 137;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 152 DSDGNATKDAAGVAGLNLALINERPAALINAVGLDTRFGKGRNVLLPDLGGGTFDSITL 211
Db 1 DSDGNATKDAAGVAGLNLALINERPAALINAVGLDTRFGKGRNVLLPDLGGGTFDSIVLT 60
Oy Db
? 212 IDGIFFREYKAT 222
| | | | | | | | | |
Db 61 IDGIFFREYKAT 71
RESULT 6
US-09-870-759-43
? SEQ ID NO 43
? PATENT NO US09870759A
? GENERAL INFORMATION:
? APPLICANT: TERPAN, David S
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
? FILE REFERENCE: 870759
? CURRENT APPLICATION NUMBER: US/09/870.759
? CURRENT FILING DATE: 2002-01-14
? PRIOR APPLICATION NUMBER: US 60/208,128
? NUMBER OF SEQ ID NOS: 50
? SOFTWARE: Patentin version 3.1
Oy Db
? SEQ ID NO 43
? LENGTH: 646
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-870-759-43
Query Match
Best Local Similarity 100.0%; Pred. No. 3.2e-42; Length 646;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 8 GIDGLTYSQGVSRHGKEVEIINDGNGNTTPSYAFDTETRLIGDAKNNOVA 60
Db 8 GIDGLTTSCGVNRHGEVEIINDGNGNKTIPSYAFDTETRLIGDAKNNOVA 60
RESULT 7
US-09-759-010-4
? Sequence 4, Application US/09759010
? Patent No. US20010034042A1
? GENERAL INFORMATION:
? APPLICANT: TERPAN, David S
? TITLE OF INVENTION: COMPLEXES OF PEPTIDE BINDING FRAGMENTS OF HEAT-SHOCK
FILE REFERENCE: 8449-135
? CURRENT APPLICATION NUMBER: US/09/759.010
? CURRENT FILING DATE: 2001-01-12
? NUMBER OF SEQ ID NOS: 11
? SOFTWARE: Patentin Ver. 2.1
Oy Db
? SEQ ID NO 4
? LENGTH: 646
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-759-010-4
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Query Match 8.38: Score 53; DB 10; Length 646;
 Best Local Similarity 100.0%; Pred. No. 3.2e-42;
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 GIDGTTTCVGVFGHKEVETIANDGSKRTTSTVAFDTERLIGDAKNQVA 60
 |||||||
 DB 8 GIDGTTTCVGVFGHKEVETIANDGSKRTTSTVAFDTERLIGDAKNQVA 60

RESULT 8
 US-09-646-835-1
 Sequence 75: Application US/10108605
 Patent No. US20020160934A1
 GENERAL INFORMATION:
 APPLICANT: Broadus, Julie
 APPLICANT: Stam, Lynn
 APPLICANT: Bachman, Jane
 APPLICANT: Khamat, Kim
 APPLICANT: Khamat, Kim
 TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND GROWTH OF DROSOPHILA MELANOGASTER THAT ENCODE
 FILE REFERENCE: 31138
 CURRENT APPLICATION NUMBER: US/10/108,605
 CURRENT FILING DATE: 2002-03-27
 PRIOR APPLICATION NUMBER: US 09/761,142
 PRIOR FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: US 60/176,418
 PRIOR FILING DATE: 2000-12-14
 NUMBER OF SEQ ID NOS: 361
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 75
 LENGTH: 651
 TYPE: PRT
 ORGANISM: Drosophila melanogaster
 US-10-108-605-75

Query Match 8.38: Score 53; DB 9; Length 651;
 Best Local Similarity 100.0%; Pred. No. 3.2e-42;
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 GIDGTTTCVGVFGHKEVETIANDGSKRTTSTVAFDTERLIGDAKNQVA 60
 |||||||
 DB 8 GIDGTTTCVGVFGHKEVETIANDGSKRTTSTVAFDTERLIGDAKNQVA 60

RESULT 9
 US-09-925-302-724
 Sequence 724: Application US/09925302
 Patent No. US20020044941A1
 GENERAL INFORMATION:
 APPLICANT: Smith, A.
 TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 FILE REFERENCE: PA104
 CURRENT APPLICATION NUMBER: US/09/925,302
 CURRENT FILING DATE: 2001-08-10
 PRIOR APPLICATION NUMBER: PCT/US00/05918
 PRIOR FILING DATE: 2000-03-08
 PRIOR APPLICATION NUMBER: 60/124,270
 PRIOR FILING DATE: 2000-03-12
 NUMBER OF SEQ ID NOS: 896
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 724
 LENGTH: 665
 TYPE: PRT
 ORGANISM: Homo sapiens
 NAME/KEY: SITE
 LOCATION: (2116)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: SITE
 LOCATION: (298)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-09-925-302-724

Query Match 7.38: Score 47; DB 10; Length 655;
 Best Local Similarity 100.0%; Pred. No. 1.0e-36;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 440 IYVEGERRAMTKDNMLGFFELSGIPAPRGVPLETFIDNGLIL 486
 |||||||
 DB 464 IYVEGERRAMTKDNMLGFFELSGIPAPRGVPLETFIDNGLIL 510

RESULT 10
 US-09-815-242-12058
 Sequence 12058: Application US/09815242
 Patent No. US20020061569A1
 GENERAL INFORMATION:
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Karl L.
 APPLICANT: Eyskild, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Trevelly, John D.
 APPLICANT: Trevelly, John D.
 APPLICANT: Yamamoto, Robert T.
 APPLICANT: Xu, H. Howard
 TITLE OF INVENTION: Identification of Essential Genes in
 FILE REFERENCE: ELTRA 0114
 CURRENT APPLICATION NUMBER: US/09/815,242
 CURRENT FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/151,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 NUMBER OF SEQ ID NOS: 14110
 NUMBER OF SEQ ID NOS FOR WINDOWS VERSION 4.0
 SEQ ID NO 12058
 LENGTH: 637
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
 US-09-815-242-12058

Query Match 3.58: Score 23; DB 10; Length 637;
 Best Local Similarity 100.0%; Pred. No. 8.9e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 464 IPPAPRGVPLETFIDNGLIL 486
 |||||||
 DB 462 IPPAPRGVPLETFIDNGLIL 484

RESULT 11
 US-09-864-761-35578
 Sequence 35578: Application US/09864761
 Patent No. US20020048763A1
 GENERAL INFORMATION:
 APPLICANT: Penn, Sharon G.
 APPLICANT: Rank, David R.
 APPLICANT: Rank, David R.
 APPLICANT: Rank, David R.
 APPLICANT: Rank, David R.
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 FILE REFERENCE: Aeomica-X-1
 CURRENT APPLICATION NUMBER: US/09/864,761
 CURRENT FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/180,312

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: PRIOR FILING DATE: 2000-02-04
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 2000-05-26 09/632,366
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 2000-10-04
: PRIOR APPLICATION NUMBER: GB 24263,6
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: US 60/236,559
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: PCT/US01/00666
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00667
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00664
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00669
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00665
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00668
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00663
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00662
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00661
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00670
: PRIOR FILING DATE: 2000-09-21
: PRIOR APPLICATION NUMBER: US 60/234,697
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: US 09/608,408
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: US 09/774,203
: PRIOR FILING DATE: 2001-01-29
: PRIOR APPLICATION NUMBER: US 09/774,203
: SOFTWARE SEQ ID NOS: 49117
: SEQ ID NO 35978
: LENGTH: 52
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: MAP TO AC009945.1
: OTHER INFORMATION: EXPRESSED IN HELIO, SIGNAL = 16
: OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 10
: OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 11
: OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.3
: OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 12
: OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 33
: OTHER INFORMATION: EXPRESSED IN SPLEEN, SIGNAL = 7.9
: OTHER INFORMATION: EXPRESSED IN BMDM, SIGNAL = 8.9
: OTHER INFORMATION: EXPRESSED IN P8109, EVALUATE 5.00e-22
: OTHER INFORMATION: EST_HUMAN HIT: BF2119.1, EVALUATE 7.00e-21
US-09-864-761-35578

Query Match 2.7% Score 17; DB 10; Length 52;
Best Local Similarity 100.0%; Pred. No. 47e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 470 GYGOIEVTFDIDANGIL 486
|||||
29 GYGOIEVTFDIDANGIL 45

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: TITLE OF INVENTION: PROTEINS AND THEIR USE AS IMMUNOTHERAPEUTIC AGENTS
: FILE REFERENCE: 8449-135
: CURRENT APPLICATION NUMBER: US/09/759,010
: CURRENT FILING DATE: 2001-01-12
: SOFTWARE SEQ ID NOS: 11
: SEQ ID NO 2
: SEQ ID NO 2
: LENGTH: 653
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-759-010-2

Query Match 2.5% Score 16; DB 10; Length 653;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 197 RIINEPTAAIAVAGD 186
|||||
197 RIINEPTAAIAVAGD 212

RESULT 13
US-09-919-172-54
: Sequence 54, Application US/09919172
: Patent No. US20020119463A1
: GENERAL INFORMATION:
: APPLICANT: Paris, Mary
: APPLICANT: Turner, Christopher M.
: FILE REFERENCE: P0016 US
: CURRENT FILING DATE: 2001-07-30
: CURRENT APPLICATION NUMBER: US/09/919,172
: CURRENT FILING DATE: 2001-07-28
: PRIOR APPLICATION NUMBER: 60/222,469
: PRIOR FILING DATE: 2000-07-28
: NUMBER OF SEQ ID NOS: 102
: SOFTWARE: PERL Program
: SEQ ID NOS: 654
: LENGTH: 654
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No. US20020119463A1 2993696CD1
US-09-919-172-54

Query Match 2.5% Score 16; DB 10; Length 654;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 171 RIINEPTAAIAVAGD 186
|||||
197 RIINEPTAAIAVAGD 212

RESULT 14
US-09-841-132-301
: Sequence 301, Application US/09841132
: Patent No. US20020061848A1
: GENERAL INFORMATION:
: APPLICANT: Bhalla, Ajay
: APPLICANT: Bhalla, Ajay
: APPLICANT: Roberts, Peter
: APPLICANT: Roberts, Peter
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
: TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
: FILE REFERENCE: 210121.469c8
: CURRENT FILING DATE: US/09/841,132
: CURRENT FILING DATE: 2001-04-23
: CURRENT OF SEQ ID NOS: 399
: SOFTWARE: SeqScribe for Windows version 3.0/4.0
: SEQ ID NO 301
: LENGTH: 183
: TYPE: PRT
: ORGANISM: Chlamydia

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US-09-841-132-301

Query Match 2.38; Score 15; DB 10; Length 183;

Best Local Similarity 10.08; Pred. No. 3.3e-06; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 472 POIEVTFDIDANGIL 486

DB 9 POIEVTFDIDANGIL 23

RESULT 15

US-09-815-242-11472

Sequence 11472; Application US/09815242

Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Olsen, Karl L.

APPLICANT: Zsindl, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE NUMBER: 2001-03-21

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 11110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 11472

LENGTH: 620

TYPE: PRT

ORGANISM: Helicobacter pylori

US-09-815-242-11472

OY 472 POIEVTFDIDANGIL 486

DB 464 POIEVTFDIDANGIL 478

Search completed: December 4, 2002, 16:56:53
Job time : 12 secs

>gi|347019|pir||S31716 dnaK-type molecular chaperone hsp72-ps1 - rat
 gi|56385|emb|CAA49670.1| Hsc70-ps1 [Rattus norvegicus]
 Length = 646

Score = 505 bits (1301), Expect = e-142
 Identities = 259/328 (78%), Positives = 288/328 (87%)

Query: 1 IDSLFEGIDFYTSITRARFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRI 60
 IDSL+EGIDFYTSITRARFEEL +DLFR TL+PVEKALRDAKLDK+QIHD+VLVGGSTRI
 Sbjct: 284 IDSLYEGIDFYTSITRARFEELNADLFRGTLDPEKALRDAKLDKSQIHDIIVLVGGSTRI 343

Query: 61 PKVQKLLQDFFNGRDLNKSINPDEXXXXXXXXXXXXXILMGDKSENVQDXXXXXXXXXXXXX 120
 PK+QKLLQDFFNG++LNKSINPDE IL GDKSENVQD
 Sbjct: 344 PKIQKLLQDFFNGKELNKSINPDEAVAYGAAVQAAILSGDKSENVQDLLLLDVTPLSLGI 403

Query: 121 ETAGGVMTALIKRNSTIPTKQTQIFTTYSDNQPGVLIQVYEGERAMTKDNNLLGRFELSG 180
 ETAGGVMT LIKRN+TIPTKQTQ FTTYSDNQPGVLIQVYEGERAMTKDNNLLG+FEL+G
 Sbjct: 404 ETAGGVMTVLIKRN+TIPTKQTQFTTTYSDNQPGVLIQVYEGERAMTKDNNLLGKFELTG 463

Query: 181 IPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITITNDKGRLSKEEIERMVQEAE 240
 IPPAPRGVPQIEVTFDIDANGILNV+A DKSTGK NKITITNDKGRLSKE+IERMVQEAE
 Sbjct: 464 IPPAPRGVPQIEVTFDIDANGILNVSADVDKSTGKENKITITNDKGRLSKEDIERMVQEAE 523

Query: 241 KYKAEDDEVQRRERSAKNALESYAFNMKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDA 300
 KYKAEDE QR++VS+KN+LESYAFNMK+ VEDE L+GKI++ DK+K+LDKC E+ISWLD
 Sbjct: 524 KYKADEKQRDKVSSKNSLESYAFNMKATVEDEKLQGKINDEDKQKILDKCNEIISWLDK 583

Query: 301 NTLAEKDEFEHKRKELEQVCNPIISGLY 328
 N AEK+EFEH++KELE+VCNPII+ LY
 Sbjct: 584 NQTAEKEEFEHQQKELEKVCNPIITKLY 611

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